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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 25, 2004, 10:42:39; Search time 59 Seconds (without alignments) 1896.421 Million cell updates/sec Run on:

US-10-667-442-2 2104 1 MGANTSRKPPVFDENEDVNF......NLALEQTKDPQGEDGQNNNL 396 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A\_Geneseq\_29Jan04:\* l:\_geneseqp1980s:\* Database :

genesequ1990s: genesequ2000s: genesequ2002s: genesequ2002s: genesequ2003bs: genesequ2003bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMADIRS

		d			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ΙD	Description	
-	2104	100.0	396	9	ABG70700	Abq70700 Human ser	
7	2104	100.0	396	9	ABU62276	Human	
m	2089	99.3	396	4	AAB85491	Aab85491 Human pro	
4	2089	99.3	396	Ŋ	AAE14261	Aae14261 Novel hum	
S	2089	99.3	396	Ŋ	AAE21725	Aae21725 Human PKI	
9	2083	99.0	396	Ŋ	AAM50334	Human	
7	2047	97.3	407	ഹ	AAE14260		
60	1500.5	71.3	327	4	AAU03504	Aau03504 Human pro	
σ	1427	67.8	404	9	ABU62277	Abu62277 Mouse ser	
10	1425.5	67.8	403	9	ABU62278	Abu62278 Human ser	
11	1425.5	67.8	414	4	AAB65600		
12	1425.5	67.8	414	ß	ABP43807	Abp43807 Serine/th	
13	1425.5	67.8	414	ഗ	AA017710	Aao17710 Human ser	
14	1425.5	67.8	414	ø	ABR58617	Abr58617 Human can	
15	1425.5	67.8	414	7	ADE38375		
16	1325	63.0	419	4	AAB65599	Aab65599 Novel pro	
17	1321	62.8	425	4	AAM40592	Aam40592 Human pol	
18	1318	62.6	485	'n	AAE24141	Aae24141 Human kin	
19	1317.5	62.6	384	9	ABU62279	Abu62279 Mouse ser	
20	1317.5	62.6	488	ഹ	AA017709	Aao17709 Murine se	
21	1315	62.5	419	4	AAM38806	Aam38806 Human pol	
22	1302	61.9	488	9	AB014992	Abo14992 Human NOV	
23	1285.5	61.1	713	Ŋ	ABB06090	Abb06090 Human NS	
24	1278.5	60.8	399	S	ABB84300	Abb84300 Murine se	
25	1259.5	59.9	375	4	AAE04371	Aae04371 Human kin	

218. .221 \_\_\_/label= Amidation\_site

Modified-site

	Human	Abu58685 Human PRO	Abu88233 Novel hum	Abu84548 Human sec	Abr66422 Human sec	Abr65812 Human sec	Abu99752 Human sec	Human	Abu90112 Novel hum	Abr68361 Human sec	Abu96414 Novel hum	Human	Human	Abo02974 Human sec	Abr75128 Human sec	Abr94890 Human sec	Human	Abu99023 Novel hum	Abu98238 Novel hum	Abu91944 Novel hum
_	AAU29309	ABU58685	ABU88233		ABR66422	•	ABU99752	ABU82991	ABU90112	ABR68361	ABU96414	ABU92845	ABO08922	AB002974	ABR75128	ABR94890	ABU85863	ABU99023	ABU98238	ABU91944
	364 4		-				_							364 6						_
	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1	57.1
	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5	1201.5
	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Human; kinase; serine/threonine kinase; immune response; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Serine/threonine_protein_kinase_active_site
                                                                                                                                                                                                                                                 . .7
|abel= Protein_kinase_C_phosphorylation_site
                                                                                                                                                                                                                                                                        .8
|abel= Protein_kinase_C_phosphorylation_site

    36
    1abel= Casein_kinase_II_phosphorylation_site

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label= Protein_kinase_C_phosphorylation_site

    92
    label= Casein_kinase_II_phosphorylation_site

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label= Protein_kinase_C_phosphorylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93. .195
| Jabel= Protein_kinase_C_phosphorylation_site
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|Jabel= Protein_kinase_C_phosphorylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12. 215
|abel= Casein_kinase_II_phosphorylation_site
                                                                                                                                                                                                                                                                                                         Protein_kinase_ATP-binding_region
                                                                                              Human serine/threonine protein kinase-like kinase.

    .7
    /label= N_myristoylation_site

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                                                                                                                                                                                                                                                                                                                                            3. 46
|abel= N_glycosylation_site
                                                                                                                                                                                                                                 label= N_glycosylation_site
                                                                                                                                                                                 Location/Qualifiers
                        ABG70700 standard, protein, 396 AA.
                                                                       (first entry)
                                                                                                                                                                                                                                                                                               9. .52
label=
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Modified-site
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                                                                       17-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                            Active-site
                                               ABG70700;
                                                                                                                                     enzyme.
RESULT 1
ABG70700
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The present invention relates to the isolation of a human kinase and the polynucleotide sequences encoding it. The human kinase of the invention is related to the serine/threonine kinase substanily. The gene encoding the human kinase is located on chromosome 5. The polypeptide and disease or condition mediated by a human kinase. Both the polypeptide and disease or condition mediated by a human kinase. Both the polypeptide and disease or condition mediated by a human kinase. Both the polypeptide and disease or condition mediated by a human kinase. Both the polypeptide and oblymucleotide sequences are useful as models for the development of human therapeutic agents, and as query sequences to perform a search against sequence are perform a search against sequence data bases to identify other family members of related sequences. The polypeptide is useful to raise antibodies or to elicit another immune response as a reagent in assays members of related sequences. The polypeptide is useful to raise designed to quantitatively determine levels of the protein in biological fluids, as markers for tissues in which the corresponding protein is preferentially expressed, in drug screening assays, in call-based or call preferentially expressed, in drug screening assays, in call-based or call free systems, to identify compounds that modulate kinase activity of the ability to stimulate or inhibit interaction between the kinase protein, and anotecule that normally interactes with the kinase protein, and in pharmacogenomic analysis. The polymucleotide is useful for a cativity of the human kinase gene in climical trials or in a treatment regimen, in diagnostic assays for qualitative changes in a human kinase gene expression in cells, tissues and adsease, nevertheless affects the treatment modality, as antissues and enganes in a human kinase gene expression in cells, tissues and organisms, for gene therapy whence the serine/threening produce transgence and personner control human kinase related to the serine/threening protein kinas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated human kinase peptide useful for treating disorder characterized by absence of, in appropriate or unwanted expression of the kinase protein, and as immunogens to raise antibodies.
230. .233
/label= Casein_kinase_II_phosphorylation_site
391. .396
                                                                 /label= N_myristoylation_site
                                                                                                                                                                                                                                                                                                                                                                                          Beasley EM;
                                                                                                                                                                                                                                                                                                                                                                                     Yan C, Di Francesco V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2; 174pp; English.
                                                                                                                                                                                             09-MAR-2001; 2001US-00801876
                                                                                                                                                                                                                                     09-MAR-2001; 2001US-00801876
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                                                                                                                                                                                                                                                                                YE J.
YAN C.
DI FRANCESCO V.
                                                                                                                                                                                                                                                                                                                                               BEASLEY E M.
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                                             Modified-site
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(YANC/)
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(BEAS/)
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ERNEVRAVFKELQIMQGLEHPFLVNLWYSPQDEEDMFWVVDLLLGGDLRYHLQQNVHFKE 120
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                                                                                                    ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRBTQITTM
                                                                                                                                           181 AGTKPYMAPEMPSSRKGAGYSPAVDWMSLGVTAYELLRGRRPYHIRSSTSSKEIVHTPET
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Best Local Similarity 100.
Matches 396; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                   ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 NKGRLNCDPTFELBEMILESKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLDSVQKRFI 360
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designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; or as markers for tissues in which the corresponding protein is preferentially expressed. The agents identified are useful for treating a subject with a disorder mediated by kinase pathway. The present sequence represents the amino acid sequence of a human kinase
                                                                                                                                                                                                                                    1 MGANTSRKEPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
                                                                                                                                                                                                                                                                                  61 BRNBVRNVPKELQIMQGLEHPPLVNLWYSPQDEEDMFWVDLLLGGDLRYHLQQNVHPKE
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100.0%; Pred. No. 8.1e-194;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2001 (first entry)
                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 396; Conservative
                                                                                                                     Sequence 396 AA;
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2000US-0179364P. 2000US-0183173P. 2000US-0190162P. 2000US-0193404P. 2000US-0247013P.

17-MAR-2000; 2 29-MAR-2000; 2 13-NOV-2000; 2

25-JAN-2001; 2001WO-US002337

02-AUG-2001

25-JAN-2000; 31-JAN-2000; 17-FEB-2000;

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The invention provides human protein kinases and protein kinase-like enzymes and polymucleotides are useful for treating a disease or colypeptides and their modulators are useful for treating a disease or disorder such as cancers of hematopoietic cardiovascular disease, brain or neuronal-associated disease and metabolic disorders, including cancers of thematopoietic origin, diseases of the cancers of hematopoietic origin, diseases of the cancers of hematopoietic origin, diseases of the cancers of hematopoietic origin, diseases of the cancers and set of hematopoietic origin, diseases of the partipheral nervous system.

Cancers and set of set of hematopoietic origin, diseases of the cancers of the partipheral nervous system.

Alzheimer's disease, Parkinson's disease, migraines pain, sexual dysfunction, acteria and fungi, ocular diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, cancers and organ transplant rejection. They are also useful for treating rhintis, autoimmunity, atherosolerosis, psoriasis, osteoarthritis, asthma, chronic inflammatory pelvic disease, chronic inflammatory bowel disease, rheumatory pelvic diseases uch as diabetes, obesity, cardiovascular diseases such as diabetes, cornary thrombosis, clotting disorders and atherosolerosis, cullur, cornary thrombosis, clotting disorders and atherosolerosis, cullur diseases such as glaucoma, retinopathy and macular degeneration, psychiatric and neurological disorders such as anxiety, schlzophrenia, cemental, manic depression, etc. The polymucleotides are useful in gene therapy techniques to treat the above mentioned disorders. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AGTKPYMAPEMFSGRKGAGYSFAVDWWSLGVTAYBLLRGRRPYHIRSSTSSKEIVHTFET 240
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                                                                                                                                                                   Kinase polypeptides useful for treating cancers, Alzheimer's disease, viral infections, diabetes, obesity, organ transplant rejection and rheumatoid arthritis.
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99.5%; Pred. No. 2.3e-192;
iive 1; Mismatches 1;
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                                                              Sudarsanam
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                                                            Manning
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                                                              Whyte D,
                                                                                                       2001-476202/51
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Best Local Similarity
                      (SUGE-) SUGEN INC.
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                                                                 Plowman G,
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             AGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKBIVHTFET
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/note= "Protein kinase domain"
23. .300
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/note= "Protein kinase domain"
25. 268
/note= "Protein kinase domain"
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22-SEP-2000; 2000US-0234902P.
29-SEP-2000; 2000US-0236499P.
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08-SEP-2000; 2000US-0231357P.
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13-OCT-2000; 2000US-0240542P-
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Burford N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel human protein (MHP) kinases and their corresponding cDNA molecules. MHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as the reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. MHP DNA is useful in the treatment of breast cancer and prostate cancer. MHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or disease, and cosmetic and nutriceutical applications. MHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular of coding sequence and the mapping of a unique gene to a particular screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPB or inappropriately expressed NHPB for disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase which is similar to serine/threonine protein kinases, ribosomal protein kinases and cAMP-capped and capped and c
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                                                                                                                                                                               Novel human protein; NHP; gene therapy; diagnosis; drug screening; gene expression; breast cancer; prostate cancer; nutriceutical; cosmetic; medical disorder; mental; biological; physiological; chemotherapeutic.
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99.3%; Score 2089; DB 5; Length 396;
Best Local Similarity 99.5%; Pred. No. 2.3e-192;
Matches 394; Conservative 1; Mismatches 1; Indels C
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                                                                                                                                              Novel human protein (NHP) kinase #4.
                                 AAE14261 standard; protein; 396 AA.
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                                                                                                                                                                                                                                                                                                                                                                             24-APR-2001; 2001WO-US013149.
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                                                                                                          (first entry)
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N-PSDB; AAD23679.
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Human; kinase; enzyme; PKIN-20 protein; immune system disorder; anaemia; acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease; asthma; neurological disorder; epilepsy; Charcot-Tarie-Tooth disease; AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder; Down's syndrome; gene therapy; protein therapy; cytostatic.
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/note= "Eukaryotic protein kinase domain"
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The present invention relates to human kinases (PKIN) and polymucleotides encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease, anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marieroth disease or seizures), cell proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, meloma, sarcoma), and developmental disorders (e.g. Down's syndrome). They are also used in gene therapy and protein therapy. The present sequence is human PKIN-20
                                                New human kinases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia or lymphoma).
                                                                                                                                                                                Claim 75; Page 184-185; 218pp; English.
N-PSDB; AAD34317.
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Sequence 396 AA;

ö 120 BRNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKE 120 240 240 BTVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180 180 TVVTYPSAWSQEMVSLLKKILEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIP 300 NKGRINCDPTFELEEMILESKPLHKKKKKRLAKKEKOMRKCDSSQTCLLQEHLDSVQKEFI 360 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGKVCIVQRNDTKGMYAMKKNKKCV 60 ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV ERNEVRIVEKELQIMQGLEHPPLVNLWYSPQDEEDMFWVVDLLLGGDLRYHLQQNVHFKE AGTKPYMAPEMPSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKBIVHTFET 181 AGTKPYMAPEMPSSRKCAGYSPAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET 241 TVVTYPSAWSQEMVSLLKKTLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIP 0; Gaps Score 2089; DB 5; Length 396; Pred. No. 2.3e-192; 1; Mismatches 1; Indels C I FINEKVIRDENKROPNIALEOTKOPOGEDGONNIL 396 I FNREKVNRDFNKRQPNLALEQTKDPQGEDGQNNNL 396 99.3%; 99.5%; Query Match
Best Local Similarity 99.57
Matches 394; Conservative 61 121 181 241 361 61 301 361 8 ठ g ð 셤 ò 셤 ઠ g ò g ò 셤

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Protein kinase; human; signal transduction; lung cancer; colon cancer;
                                                                                      brain cancer; breast cancer; therapy; diagnosis.
                                                                                                                       Location/Qualifiers 2. .7
AAM50334 standard; protein; 396
                                                          Human 14911 protein kinase.
                                                                                                                             Key
Modified-site
                                      04-FEB-2002
                   AAM50334;
                                                                                                           Ношо
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transduction of signals for cell proliferation, differentiation and transduction of signals for cell proliferation, differentiation and apaptosis, modulating the activity of one or more proteins involved in cellular growth or differentiation. 1991 molecules are overspressed in some tumour cells, where they may inappropriately propagate either cell proliferation or cell survival signals. The invention provides methods for the diagnosis and treatment of cancer, including breast colon, brain and especially lung cancer (claimed), and methods for evaluating the efficacy of treatment. 14911 polypeptides can be produced by cultivation of claimed host cells, and used in claimed methods of identifying 14911 modulator compounds. 14911 binding partners are used in claimed methods of identifying subjects at risk of cancer or cellular proliferation and/or differentiation disorders. A claimed method of treating cancer or

present sequence is that of a novel human protein kinase, designated

Claim 4(d); Fig 1A-B; 115pp; English.

modulators.

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Novel protein kinase nucleic acid molecules and the encoded proteins for diagnosing and treating cellular proliferative, bone, immune, cardiovascular, liver, pain or metabolic disorders and identifying
                                                                           "protein kinase ATP-binding region signature"
                            ...7
note= "O-phosphorylated by protein kinase C"
                                                                                                                 "O-phosphorylated by protein kinase C"
                                                                                                                                   "O-phosphorylated by casein kinase II"
                                                                                                                                                       "O-phosphorylated by protein kinase C"
                                                                                                                                                                                             "O-phosphorylated by protein kinase C"
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230. .232
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horte= "O-phosphorylated by casein kinase
218. .221
/note= "Amidated"
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282. 301
/label= Protein_kinase_C-terminal_domain
                  note= "Asn is N-glycosylated"
                                                                                              "Asn is N-glycosylated"
                                                       /label= Protein_kinase_domain
29. .37
                                                                                                                                                                         /note= "active site signal"
/note= "N-myristoylated"
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15-JUN-2000; 2000US-00593927.
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45. .47
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                                                . 281
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                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene expression; breast cancer; prostate cancer; nutriceutical; cosmetic; medical disorder; mental; biological; physiological; chemotherapeutic.
                                                                                                                                                                                                                                                                                   ERNEVRIVEKELQIMQGLEHPFLVILMYSFQDEEDMFMVVDLLLGGDLRYHLQQIVVHFKE 120
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               lung, colon, brain and breast cancer, uses a small molecule, peptide, phosphopeptide, anti-14911 antibody, a 14911 polypeptide or its variant. Other disorders that may be diagnosed/treated include those associated with bone metabolism, autoimmune diseases, cardiovascular disorders, liver disorders, viral diseases, pain and metabolic disorders
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a cellular proliferation and/or differentiation disorder, especially
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                                                                                                                                                 Length 396;
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                                                                                                                                              99.0%; Score 2083; DB 5;
99.2%; Pred. No. 8.6e-192;
iive 1; Mismatches 2;
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01-MAY-2000; 2000US-0201227P.
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                                                                                                                                                                             Matches 393; Conservative
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N-PSDB; AAD23678.
                                                                                                                                                                 Best Local Similarity
                                                                                                                  Sequence 396 AA;
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corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as bharmaceutical reagents useful in the therapeutic treatment of mental biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and nutriceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPB or inappropriately expressed NHPB for sequence is novel human protein (NHP) kinase which is similar to and an analyses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 BIVKLFICELVMALDYLQNQRIIHRDMKPDNILLDBHGHVHITDFNIAAMLPRBTQITTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                  The invention relates to novel human protein (NHP) kinases and their
                  New nucleic acid molecules encoding new human proteins, useful in diagnosis, drug screening, clinical trial monitoring, treatment of physiological disorders, and cosmetic or nutriceutical applications.
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                                                                                                         Claim 5; Page 41-42; 44pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polymucleotides encoding protein kinases and the polymorpides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of hemanopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. theumatoid arthritis), neurological disorders (e.g. achizophrenia), neurodespenerative disorders (e.g. chanson's disease), inflammatory disorders (e.g. asthma), infectious disorders (e.g. HIV) and reproductive disorders (e.g. infectility).

Additionally, polymucleotides encoding protein kinases may be used as antigens in the production of antibodies against the protein kinase such in assays to identify modulators of protein kinase expression and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVTAYBLLRGRRPYHIRSSTSSKEIVHTFET 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLFRETQITTM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSPQDEEDMFWVVDLLLGGDLRYHLQQNVHFKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSPQDEEDMFMVVDLLLGGDLRYHLQQNVHFKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVVTYPSAWSQEMVSLLKKLLE----PNPDQRFSQLSDVQ---NFPYMNDINWDAVFQKR 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVVTYPSAWSQEMVSLLKKVRRKTACPNEVTKGSRLSGLSLEVSIQY-----WGHQLSSL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGKVCIVQKNDTKKMYAMKYMNKQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.3%; Score 1500.5; DB 4; Length 327; 87.0%; Pred. No. 9.1e-136; ive 6; Mismatches 19; Indels 19;
                                                                                                                                                                                                                                                                                Manning G, Sudarsanam S, Martinez R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QKGRINCDPTFELEEMILESKPLHKKKKKLAK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Fig 2; 433pp; English.
                                                                                                                                                              22-NOV-2000; 2000WO-US032085.
                                                                                                                                                                                                   99US-0167482P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 87.0
Matches 295; Conservative
                                                                                                                                                                                                                                                                              Whyte D,
Clary D;
reproductive disorder.
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-343950/36.
N-PSDB; AAS06704.
                                                                                                                                                                                                                                         (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 327 AA;
                                                                             WO200138503-A2
                                                                                                                                                                                                 24-NOV-1999;
                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                   Flanagan P,
                                                                                                                                                                                                                                                                                Plowman GD,
                                                                                                                      31-MAY-2001
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C. The invention relates to a new isolated human kinase peptide. The human kinase peptide and nucleic acid molecules are useful in the development of kinase peptide and nucleic acid molecules are useful in the development of the mann therapeutics and diagnostic compositions. The peptides are useful for treating disorders (e.g. cancers, inflammations, carteriosclarosis or psoriasis) characterised by an absence of, inappropriate, or unwanted avgression of the kinase protein. These molecules are particularly useful as models for developing human therapeutic proteins, or serving as therapeutic targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The peptides are also useful for raising antibodies or eliciting an immune compones, as a reagent (including the labelled reagent) in assays response to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; or as markers for tissues in which the corresponding protein is preferentially expressed. The agents identified are useful for treating a subject with a disorder mediated by kinase pathway. The present sequence represents the amino corresponding protein kinase #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human kinase proteins, useful for treating disorders mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis or psoriasis), or for development of human therapeutics and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 - ERNEYRNYFKELQIMQSLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITT 179
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                                                                                                                                                                                                                                                                                                Mouse; enzyme; kinase; gene therapy; cancer; inflammation; psorlagis;
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69.5%; Pred. No. 1.5e-128;
ive 38; Mismatches 64; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beasley EM;
                                                                                                                                                                                                                      Mouse serine/threonine protein kinase #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 2B; 185pp; English.
ABU62277 standard; protein; 404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Di Francesco V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2002; 2002US-00254869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-2001; 2001US-00801876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003027307-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compositions.
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
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                                                                             ABU62277;
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Sequence 403 AA;

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the invention relates to a new isolated human kinase peptide. The human kinase peptide and nucleic acid molecules are useful in the development of human therapeutics and diagnostic compositions. The peptides are useful for treating disorders (e.g. cancers, inflammations, arteriosclerosis or psoriasis) characterised by an absence of, inappropriate, or unwanted expression of the kinase protein. These molecules are particularly useful as models for developing human therapeutic targets, identifying therapeutic proteins, or serving as therapeutic targets for the development of human therapeutic proteins, or serving as targets for the development of human therapeutic gents that modulate kinase activity in cells and tissues that express the kinase. The peptides are also useful for raising antibodies or eliciting an immune response, as a reagent (including the labelled reagent) in assays response, as a reagent (including the labelled reagent) in assays response to rigand) in biological fluids, or as markers for tissues in which the corresponding protein is preferentially expressed. The agents identified are useful for treating a subject with a disorder mediated by kinase pathway. The present sequence represents the amino acid sequence of the human serine/threonine protein kinase #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human kinase proteins, useful for treating disorders and landlated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis or psoriasis), or for development of human therapeutics and diagnostic compositions.
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                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                        PIPNKGRINCDPTPELBEMILESKPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDSVQ 356
                                                                                                                                                                                                                                                                                                                                                                                    EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVLKGSEKASS 180
                                                                    237
                                                                                                        PETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNPPYMDINWDAVFQKRLIPG
                                                                    MAGTKPYMAPEMPS -- SRKGAGYSPAVDWWSLGVTAYELLRGRRPYHIRSSTSSKRIVHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEPII PNREKVNRDFNKRQPNLALEQTKDPQGEDGQNNNL 396
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121
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ABU62278
ID ABU62
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                                                                                                                            BRNEVRNVFKELQIMQGLEHPPLVNLWYSPQDEEDMFWVVDLLLGGDLRYHLQQNVHFKE 120
                                                                                                                                                                                                                                                                                                                                                                                      299 IPNKGRINCDPTFELBEMILESKPLHKKKKRLAK-KGKOMRKCDSSQTCLLQEHLDSVQK 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antinflammatory; antiasthmatic; dermatological; antidabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.
                                                                                                                                                121 BTVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM
                                                                                                                                                                                                              121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVVKGAERASSM
                                                                                                                                                                                                                                                                                                                                          241 KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDAVFKKALMPGF
                                                               1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
                                                                                                                                                                                                                                                                         1 MGGNHSHKPPVFDENBEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKKQKCI
                                                                                                                                                                                                                                                          181 AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTF
                                 Gaps
                                                                                                                                                                                                                                                                                                                         239 BTTVVTYPSAMSQEMVSLLKKTLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGF
                              7;
   Length 403;
67.8%; Score 1425.5; DB 6; Length
68.2%; Pred. No. 2.1e-128;
.ive 44; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 BFIIFNREKVNRDFNKROPNLALEQTKOPQG----EDGONNNL 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel protein kinase, SEQ ID NO: 125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB65600 standard; protein; 414 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0136503P
                  Best Local Similarity 68.2%
Matches 275, Conservative
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N-PSDB; AAF44625.
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   Query Match
Best Local 8
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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression cuch as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune cisorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, proriasis, rhinitis, autoimmulty, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRNEVRIVVPKELQIMQGLEHPFLVNLWYSPQDEEDMFWVVDLLLGGGDLRYHLQQNVHFKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERDEVRIVVERELQIMOGLEHPFLVNIMYSFQDEEDMFWVDLLLGGDLRYHLQQNVHFTE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPNKGRLNCDPTFELBEMILESKPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDSVQK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGGNHSHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMKQKCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVVKGABRASSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKRIVHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETTVVTYPSAMSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      67.8%; Score 1425.5; DB 4; Length 414; 68.2%; Pred. No. 2.2e-128; ive 44; Mismatches 77; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFIIFNREKVNRDFNKROPNLALEQTKDPOG----EDGONNNL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 BFIIFNREKLRRQQQQSQLLDTDSRGGGQAQSKLQDGCNNNL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP43807 standard, protein; 414 AA
                 Claim 10; Fig 1; 310pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 275; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Neuroprotective; immunomodulator; cancer; chromosome 4p16.1-p14; cytosbtatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
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61 BRDEVRNVPRELQIMQGLEHPFLVNLMYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTE 120

121 GTVKLYICELALALEYLQRYHIHRDIKPDNILLDEHGHVHITDFNIATVVKGABRASSM

121 BTVKLFICELVWALDYLQNQRIIHRDWKPDNILLDBHGHVHITDFNIAAMLPRETQITTM

**ETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGF** 

239

AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYBLLRGRRPYHIRSSTSSKBIVHTF

181

셤 ઠ 셤 8 셤 ò

180

9 9

7; Gaps

1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV 1 MGGNHSHKPPVFDENBEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMNKQKCI 61 ERNEVRAVPKELQIMQGLEHPFLVALWYSPQDEEDMFMVVDLLLGGDLRYHLQQAVHFKE

> 셤 ઠે 셤 8 셤

Query Match 67.8%; Score 1425.5; DB 5; Length 414; Best Local Similarity 68.2%; Pred. No. 2.2e-128; Matches 275; Conservative 44; Mismatches 77; Indels 7;

300

299 IPNKGRLNCDPTFELEEMILESKPLHKKKKRLAK-KRKDMRKCDSSQTCLLQEHLDSVQK 357

358 BFIIFNREKVNRDFNKRQPNLALEQTKDPQG----BDGQNNNL 396 EFIIFNKEKLRRQQGQGSQLLDTDSRGGGQAQSKLQDGCNNNL 403

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The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, vulnerary, neuroprotective, immunomulator, cytostatic and antinifiammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABP4359 represent polypeptides encoded by polynucleotides of the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/bublished_pct_sequences
                                                                                                                                                                                                                                                                                                                                  New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
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                                                                                                                                                                                                                     Ren
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID # 710; 357pp + Sequence Listing; English
                                                                                                                                                                                                                   Zhao QA,
                                                                                                                                                                                                              Tang YT, Liu C, Zhou P, Asundi V, Zhang J,
Kue AJ, Yang Y, Wehrman T, Drmanac RT;
                                                                                                 11-OCT-2001; 2001WO-US027760.
                                                                                                                                      12-OCT-2000; 2000US-00687527
                                                                                                                                                                                                                                                                             WPI; 2002-426278/45.
                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                             N-PSDB; ABQ61051.
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                      WO200231111-A2
                                                         18-APR-2002
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ä,
                                                                                                                                                                           Human, serine-threonine protein kinase, cancer; diabetes, obesity, central nervous system disorder; inflammation; gene therapy; COPD; neuroprotective; cytostatic; anciparkinsonian; cerebroprotective; cytostatic; antidialergic; antiasthmatic; antidepessant; anorectic; antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGGDLRYHLQQNVHFKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDEVENVERELGINGGLEHPFLYNLMYSPQDEEDMFMVVDLLLGGEDLRYHLQQNVHFTE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITIM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GTVKLYICELALALEYIQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVVKGAERASSM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETTVVTYPSAWSQEMVSLLKQZLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a human serine-threonine protein kinase. The sequences can be used in the diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or traumatic brain injury), diabetes, eating disorders (e.g. obesity, anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and chronic obstructive pulmonary disease (COPD). The present sequence is a human serine-threonine protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human serine-threonine protein kinase and encoding polynucleotides, useful for diagnosing, treating and preventing central nervous system disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGANTSRKPPVFDENEDVNFDHFB1LRA1GKGSFGEVC1VQKNDTKKMCAMKYMNKQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGGNHSHKPPVPDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKK9YAMKYMNKQKCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.8%; Score 1425.5; DB 5; Length 414; 68.2%; Pred. No. 2.2e-128; ive 44; Mismatches 77; Indels 7;
                                                                                                                                            fuman serine-threonine protein kinase #2.
                                AA017710 standard; protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Pig 8; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2000; 2000US-0240097P.
                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-2001; 2001WO-EP011892.
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.2°
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-435534/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 414 AA;
                                                                                                                                                                                                                                                                                                                                               40200233056-A2
                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                        20-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                   25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koehler RH;
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RESULT 13
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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or downcomprises the sequence of any of the genes that are up-regulated in specific cancers (e.g. about 1031 genes up-regulated in capulated in specific cancers (e.g. about 1031 genes up-regulated in capulated in specific cancers (e.g. about 1031 genes up-regulated in capulated gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising the vector; (4) an isolated polypeptide, which is encoded by comprising the vector; (4) an isolated polypeptide, which is encoded by comprising the vector; (5) an extibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a companient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a companient of the appropriate and (6) and (7) 
                                                                           299 IPNKGRINCDPTFELEEMILESKPLHKKKRRLAK-KEKDMRKCDSSQTCLLQEHLDSVQK 357
                                                                                                          301 VPNKGRLNCDPTFELBEMILESKPLHKKKKRLAKNRSRDGTKDSCPLNGHLQHCLETVRE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genes that are up-regulated or down-regulated in cancers, useful a
markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
therapeutic targets for screening drugs for treating these diseases.
241 KVERVHYSSTWCKGMVALLRKLLTKDPBSRVSSLHDIQSVPYLADMMPAVFKKALMPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hevezi PA, Mack DH, Wilson KB;
                                                                                                                                                                                                                             Briifnreklrroggggggglldtdsrgggagsklogggnnnl 403
                                                                                                                                                                              BFIIFNREKVNRDFNKROPNLALEQTKDPQG----BDGQNNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer related protein SEQ ID NO:274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 748; 767pp; English
                                                                                                                                                                                                                                                                                                                                                          ABR58617 standard; protein; 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0323887P.
2001US-0350666P.
2002US-0355145P.
2002US-035257P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-2002; 2002WO-US029560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gish KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ACC72764
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08-FEB-2002;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                121 GTVKLYICELALALEYLQRYHIHRDIKPDNILLDEHGHVHITDFNIATVVKGAERASSM
                                                                                                                                                                                                                                             tumourigenic disorder; angiogenic disorder; aberrant gene expression; aberrant protein activity; oytostatic; antithyroid; antidiabetic; ophthalmological; cancer; breast cancer; colon cancer; lung cancer; prostatic cancer; drawe's disease; diabetic retinopathy; protein 3703.
                                                                                                     ETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGF
                                                                                                                                                                                                                                                                                          1 MGANTSRKPPVFDENEDVNFDHPEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
                                                                                                                                     ERNEVRNVPKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKE
                                                                                                                                                                                  ETVKLFI CELVMALDYLQNQRI IHRDMKPDNI LLDEHGHVHI TDFNI AAMLPRETQITTM
                                                                                                                                                                                                                               AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYBLLRGRRPYHIRSSTSSKEIVHTF
                                                                   Gape
                                                                   7;
                                              DB 6; Length 414;
                                            67.8%; Score 1425.5; DB 6; Length
68.2%; Pred. No. 2.2e-128;
ive 44; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                      EFIIFNREKVNRDFNKRQPNLALEQTKDPQG----EDGQNNNL 396
                                                                                                                                                                                                                                                                                                                                                                                      BELLENREKGERROGGGGGGLIDTBSRGGGGAGSKLODGGNNNL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein 3703 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE38375 standard; protein; 414 AA
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2002US-0388853P.
2002US-0389395P.
2002US-0391324P.
2002US-0395944P.
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2002US-0364517P.
2002US-0371075P.
2002US-0371507P.
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2002US-0374194P.
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                                                                  Matches 275; Conservative
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09-APR-2002;
16-APR-2002;
16-APR-2002;
19-APR-2002;
31-MAY-2002;
31-MAY-2002;
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25-JUN-2002;
15-JUL-2002;
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This invention relates to a novel method of treating a human subject having a tumourigenic disorder or angiogenic disorder, caused by aberrant gene expression or activity of an isolated protein, by administering a modulator. The modulator may have cytostatic, antithyroid, antidiabetic or ophthalmological activity. The method is useful for treating a subject having a tumourigenic or angiogenic disorder, in particular for treating cancer (for example breast cancer, colon cancer, lung cancer or prostatic cancer) and, for example, Grave's disease and diabetic retinopathy. The present sequence is the amino acid sequence of the novel isolated human protein 3703 of the invention.
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                                                                                                                                                                       Hunter JJ, Macbeth KJ, Tsai F, Williamson MW, Rudolph-Owen LA;
              22-AUG-2002; 2002US-0405155P.
27-AUG-2002; 2002US-0405161P.
25-COT-2002; 2002US-0421195P.
19-NOV-2002; 2002US-0425456P.
10-DEC-2002; 2002US-0435426P.
2002US-0403046P
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Matches 275; Conservative
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N-PSDB; ADE38374.
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Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730009C22 product:SIMILAR TO SERINE
THREONINE KINASE 32 homolog [Homo sapiens], full insert sequence.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Managawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, UKL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
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THREONINE KINASE 32 homolog [Homo sapiens] (SPTR|AAH21666,
evidence: FASTY, 95.5%ID, 94.5%length, match=471)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 1927)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S.
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Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Taurumi-ku, Yokohama, Ranagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
Exx:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.

URL:http://fantom.gsc.riken.go.jp/.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Thote="unnamed protein product; SIMILAR TO SERINE
THREOHIEX KINASE 32 homolog [Homo saplens] (SPTR|AMH21666,
evidence: PASTY, 95.5%ID, 94.5%length, match=471)
                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., 18hii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamanuco, R., Matsunco, H., Sakaguchi, S., Ikegami, T., Kashiwai, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Haysshizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase II Team and the
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/mol type="mRNA"
/strain="CS7BL/6J"
/db_xref="FANTOM DB:A930015B13"
/db_xref="MG1:2409788"
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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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                                                       CGACCAAAGGAGGCTCAATTGTGACCCCCACTTTTGAACTGGAAATGATTTTGGAGT 1313
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
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Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630050F05 product:SIMILAR TO SERINE THREONINE KINASE 32 homolog [Homo saplens], full insert sequence. AK036266.1 GI:26331271 HTC; CAP trapper. Mus musculus (house mouse)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                       1090 ACATGAGTGACATGAACTGGGACGCCGTCCTGCAGAAGAGGCTCATTCCAGGCTTCATTC
                                               CTAATAAAGGCAGGCTGAATTGTGATCCTACCTTTGAACTTGAGGAAATGATTTTGGAGT
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                                                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, J., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yonada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
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Matches 1218; Conservative 0; Mismatches 245; Indels
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Thote="unmamed protein product; SIMILAR TO SERINE
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evidence: PASTY, 95.5%ID, 94.5%length, match=471)
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Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 893)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki CDNA Library Arrayed by: Th.M. CDNA Library Arrayed by: The T.M. A.G. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLnM10041 row: h column: 24
High quality sequence stop: 764.
Location/Qualifiers
                                                                                                                                                                                                                         /mol_type="mmm"
/db_xref="taxon:9606"
/clone="lmdGB:4375751"
/tissue_type="hippocampus"
/lab_host="DH108"
                                                                                                                                                                                                     organism="Homo sapiens"
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	URL:http://fantom.ggc.riken.go.jp/.  Ess Location/Qualifiers 1. 3439  Ource   organism="Mus musculus"   mol.type="mrxNa"     db_xref="RANTOM_DB:C230053G02"     db_xref="RANTOM_DB:C230053G02"     db_xref="reacon:10090"     clone="C230053G02"     tissue type="cerebellun"     clone="C230053G02"     tissue type="cerebellun"     clone="Ib="RIKEN full-length enriched mouse cDNA library"     dev_gtage="0 day neonate"	3691613  Jobce="unnamed protein product; putative serine threonine kinase 32 (MGD   MGI:1927552, GB   AJ250840, evidence: BLASIN, 99%, match=1955)"  /codon start=1	HRSRDSTKDSCK SKLQDGRNNNII 3430, 7note="putat te 3439 /note="putat /note="putat	Similarity 69.9%; Pred. No. 1.1e-94; 1; Conservative 0; Mismatches 328; 1 ATGGGAGCGAACACTTCAAGAAAACCACCAGTGTTTGATGAE	63 GACCACTTTGAAATTTTGCGAGCCATTGGGAAAGGCAGTTTTGGGGAGGTCTGCATTGTA 122  [	GAGCGCAATGAAGTGAAATGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGGACTCGGAGGACTCTGAAGGAACTCCAGATCATGCAGGGTCTGGAGGACTCTGAAGGAACTCCAGATCATGCAGGGTTTGAAGGAACTCTTCCTTC
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89 9 6 6 9 7 2 5 6 9	AK082468 AK082468 HTC, AK082468 HTC, MMB MUSCHOOL MMB MUSCHOOL MMBMMBlia, I Carninci, High-effi Meth. Enry	AUTHORS  AUTHORS  AUTHORS  AUTHORS  AUTHORS  TICH, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  ILCH, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  TITLE  Normalization and subtraction of cap-trapper-selected cDNAs to  JOURNAL  Genome Res. 10 (10), 1617-1630 (2000)  MEDLINE  20499374  PUBBRD  11042159  AUTHORS  Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itch, M.,  Yamamoto, R., Matsumoto, H., Sakauchi, S., Ikegami, T., Kashiwaci, K.,	Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Öhara, B., Wata Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizak RIKEN integrated sequence analysis (RISA) system-384-form sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)	S AI	TITLE Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs JOURNAL Nature 420, 563-573 (2002) REFERENCE 6 (bases 1 to 3439) AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., RUNDAS,S., Puruno,M., Hanagaki,T., Hara,H., Hanagaki,T., Harayaki,T., Haray	Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kolima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Mimazaki, R., Ohno, M., Ohato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Kanisaki, Y., Muramatsu, M. and Hayashizaki, Y.

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657 GGCCGGAGACCGTATCATTCGCTCCAGTACTTCCAGCAAGAAATTGTACACACGTTT 716
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1245)
Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M. A., Tanenbaum, D. M., Civello, D. R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
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Mus musculus HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY406286
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                          Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                             Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submitsed on Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 CCCTTCCTGGTGAACCTATGGTACTCCTTCCAGGATGAGGAAGACATGTTCATGGTGGTGTG
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                                                    gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 1245
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/db_xref="taxon:10090"
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Adams, M.D. and Cargill, M.
                          TITLE
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AY406284 12-DEC-2003
Homo sapiens HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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721 AAGGTGGAGCGTGTCCACTACTCCTCCTGGTGTGAGGGGATGGTGCCCTGCTGAAG 780
                                                                                                                                                                                                                                                837 CCGTATATGAATGATATAAACTGGGATGCAGTTTTTCAGAAGAGGCTCATTCCAGGTTTC 896
                                                                                                                                                                                                                                                                                             841 ACCTACCTGGCTGACATGAACTGGGATGCAGTATTCGAGAAGGCCCTGATGCCTGGCTTT 900
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Sockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
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                                                                 GAGACGACTGTTGTAACTTACCCTTCTGCTCACAGGAAATGGTGTCACTTCTTAAA
                                                                                                                                                         777 AAGCTACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTC
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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AY406284.1 GI:39762258
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JOURNAL
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DB 29; Length 1245;

36.4%; Score 540.8;

Query Match

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GAGTCCAAACCTCTACATAAGAAAAAAAGCGTCTGGCAAAGAA---GGAGAAGGATATG 1013
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                                                                                                                                                                                                                                           63 GACCACTITGAAATTTTGCGAGCCATTGGGAAAGGCAGTTTTGGGGAGGTCTGCATTGTA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCGCAATGAAGTGAAAATGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGCAC
                                                                                                     3 ATGGGAGCGAACACTTCAAGAAAACCACCAGTGTTTGATGAAAATGAAGATGTCAACTTT
                                           Gaps
   Pred. No. 7.9e-92;
0; Mismatches 337; Indels
   69.18;
Best Local Similarity 69.1 Matches 772; Conservative
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2161 bp mRNA linear HTC 20-5EP-2003
Mus musculus adult male corpora quaddrigemina cDNA, RIKEN
Ell-length enriched library, clone:B230385A21 product:hypothetical
serine/threonine protein kinase, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  957 GAGTCCAAACCTCTACATAAGAAAAAAAAAGCGTCTGGCAAAGAA---GGAGAAGGATATG 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1014 AGGAAATGCGATTCTTCTCAGACATGTCTTCAAGAGCACCTTGACTCTGTCCAGAAG 1073
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GACCTGCTCCTGGGAGGGGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTCACAGAG 360
                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                              481 cacatracagaciticaacatraccaaccaracagaagaagaagagagarrccrccarc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 GGATACTCGTACCCTGGACTGGTGGTCCCTGGGGCTATCACAGCCTATGAGCTGCTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      897 ATTCCTAATAAAGGCAGGCTGAATTGTGATCCTACCTTTGAACTTGAGGAAATGATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901 GTGCCCAATAAAGGGAGGTTGAATTGCGATCCCACATTTGAGCTTGAAGAAATGATCTA
                                                                                                                                                                                                                                                                                                                                                                   543 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGCAGGC---
                                                                                                                                                                                                                                                                                                                                                                                                                     541 GCTGGCANNNNNNNNNNNNNCTCCAGAAGTATTCCAGGTGTACATGACGAGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TATTCCTTTGCTGTTGACTGGTGGTCCTGGGAGTGACGGCATATGAACTGCTGAGA
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                                                 GGCCGGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTT
                                                                                                                                                                                                                                                               CACATCACAGATTTCAACATTGCTGCGGATGCCCCAGGGAGACACAGATTACCACGTG
                                                                                                                                                        CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACGTG
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Mus musculus (house mouse)
Mus musculus
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1245 bp DNA linear GSS 12-DEC-2003
Pan troglodytes HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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        1021 ACAAAGGACAGCTGCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGGAG 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCATCGTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGCAC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCATGGTGGTG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1245)
Clark, A.G., Glanonski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M. Least A. M. Constant A. Const
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark. A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark. A.G., Glanowski, S., Nielson, R., Tu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ATGGGAGCGAACACTTCAAGAAAACCACCAGTGTTTGATGAAAATGAAGATGTCAACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.9%; Score 533.8; DB 29; Length
Larity 68.2%; Pred. No. 1.6e-90;
Conservative 0; Mismatches 347; Indels
                                                                                   1074 GAGTTCATAATTTTCAACAGAGAAAAGTAAACAGGGA 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                       troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                                                                                  AY406285.1 GI:39762259
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/clone_lib="RIKZN full-length enriched mouse cDNA library'
/dev siege="adult"
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/note="unnamed protein product; hypothetical serine/threonine protein kinase (LocusLink|57740, GB|MM 021302, evidence: BLASTN, 99%, match=2159) putative"
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                                                                                                                                                                             /proteIn_id="BAC32730.1"
/db_xref="GI:26338089"
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                                                                                                                                                                                                                                        Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                        Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., SaBaki, N., Carninci, P.
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Nature 409, 685-690 (2001)
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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/strain="C57BL/6J"
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744 GCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGCTACTCGAACCTAATCCAGACCAA 803
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                                                                                                                                                         1310 AAGCGGCTGGCCAAGAATAAGTCTCGGGACAGCAGCAGAGACAGTTCCCAGTCGGAGAAT 1369
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Homo sapiens
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31.4%; Score 466; DB 13; Length 829;

Query Match

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836 bp mRNA linear BST 29-NOV-2002
603155332F1 CSEQRBL05 Gallus gallus cDNA clone ChEST168p8 5', mRNA
sequence.
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Gallus gallus (chicken)
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
1 (Bases I to 885;
Boardman, P. B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                            121 TACAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAAAGTGCG 180
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                                                                                                                                                                         61 TIGACCACITIGAAAITITIGCGAGCCAITIGGGAAAGGCAGTTITIGGGGAGGTCTGCATTG 120
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                                                                       1 CCATGGGAGCGAACACTTCAAGAAACCACCAGTGTTTGATGAAAATGAAGATGTCAACT
                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simon Hubbard
Department of Blomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
98.9%; Pred. No. 1.1e-77; indels :ive 0; Mismatches 5; Indels
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Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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/organism="Homo sapiens"
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/note="Organ: breast; Nector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: breast; Notionally; oligno-dT primed.
Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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I (bases I to 68.05)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

Plate: LLAMINIA row: g column: 05

High quality sequence stop: 593.
                                                                                                                 Euteleostomi;
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  GI:12425892
                                                       Homo sapiens (human)
Homo sapiens
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BG033516
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30.7%; Score 455.2; DB 13; Length 836;
Best Local Similarity 78.1%; Pred. No. 1.1e-75;
Matches 547; Conservative 0; Mismatches 153; Indels 0;
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/mol type="mann,"
/mol type="mann,"
/db xref="taxon.9606"
/clone="inAdms:5744569"
/tissue type="medulla"
/lab_host="bH108"
/lab_host="bH108"
/clone_lib="NIH MGC_119"
/cl
                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria; Primates; Catarrhini, Hominidae, Homo.

E. (Lases 1 to 1072)

National Liptricutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Apencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiML at:

http://image.llnl.gov

Plate: LLAM12767 row: c column: 18

High quality sequence stop: 692.

Location/Qualifiers

Irce

//craniamentalion
                                 1072 bp mRNA linear EST 12-MAR-2002
AGENCOURT 6707640 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5744969
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Mus musculus (house mouse)

Mus musculus

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Enkaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mutinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Lo 724)

Mutional Lo 724)

Mutional Institutes of Health, Mammalian Gene Collection (MGC)

Thoublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: cgapbe: remail.nih.gov,

Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html

This Clone was contributed by the Brain Molecular Anatomy Project
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                                                  GACCTGCTCCTGGGGAGGCGACCTGCGCTACCATCTGCAGAATGTGCATTTCACAGAG 418
                                                                                                                              GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACCAG 422
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     /tissue_type="Mole brain"
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/note="Organ: Brain, Vector: pXX- Asc; Site_l: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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Best Local Similarity 78.4%; Pred. No. 1.3e-68;
Matches 561; Conservative 0; Mismatches 128; Indels 27; Gaps
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clone="IMAGE:6842871"
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/db_xrefe"taxon:10090"
/db_xrefe"taxon:10090"
/clone="IMAGE:6817171"
/tiseuc_type="whole brain"
/dev stage="whole brain"
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/clone=1D="NIH BMAP FW0"
/clone=1D="NIH BMAP FW0"
/clone=1D="NIH BMAP FW0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is ACGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
CA120851 711 bp mRNA linear EST 09-JUL-2003
UI-M-FW0-ccb-b-18-0-UI.rl NIH BMAP_FW0 Mus musculus cDNA clone
IMAGE:6817171 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 GATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAAAGTGCGTGGAGCGCAAT 191
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (Dases 1 to 711)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Best Local Similarity 72.8%; Pred. No. 3.7e-63;
Matches 517; Conservative 0; Mismatches 187; Indels 6;
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Location/Qualifiers
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/strain="C57BL/6"
                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                      CA320851.1 GI:24538949
                                                                                                                                                                                                                                                                            Mus musculus
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CTGGGTGGGGACCTGCGCTACCACCTACAGAGAGATGTGCACTTCACAGAGGGACCGTG 300
                                                                              AAGCCTTACATGCCACCTGAGATGTTC-----AGCTCCAGAAAAGGAGCAGGCTATTCC 605
                                                                                                                                                                                                                                             666 CCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGACGACT 725
                                 312 CTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCACTTCAAGGAAGAACAGTG 371
                                                                   372 AAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACCAGCGCATCATT 431
                                                                                                                                                                                                                                                                             726 GITGIAACTIACCCTICIGCCCGGGAAAIGGIGICACTICITAA 775
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Search completed: June 26, 2004, 23:07:47 Job time : 2836 secs

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June 26, 2004, 22:20:22 ; Search time 500 Seconds (without alignments) 13605.835 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 100, Appl Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 12, Appli Sequence 12, Appli	Sequence 231, App Sequence 239, App Sequence 6, Appli
SUMMARIES ID	US-09-801-876B-1 US-10-667-442-1 US-10-254-869-1 US-10-10-764-100 US-10-362-892-44 US-10-182-243-1 US-10-182-243-1 US-10-188-798-44 US-09-841-683-10 US-09-841-683-10 US-09-841-683-10 US-09-841-683-10	US-10-108-260A-231 US-10-276-774-239 US-09-841-683-6
	9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	13 13
% Query Match Length DB	14885 15881 15881 15984 11991 11991 11991	2063 678 711
\$ Query Match	1000 1000 1000 1000 1000 1000 1000 100	4 4 5 5 3 4 4 6 5 5 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
Score	1485 1485 1485 1228 6 1188 2 1188 2 1186 2 11186 6 11160 6	1029.4 672.8 656.2
Result No.	10 w 4 m 6 7 m 6 0 11 d 6	12 13 14

TACAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAAAGTGCG 180

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11.7 M 4.07 M 5.07 M 5.	, AND	<sub>Барв</sub>	CAACT	ATTG
Sequence	PROTEINS.	65;	GATGT	ttgaccactitgaaaitttgcgagccaitgggaaaggcagtittggggaggtctgcaitg 
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		Length 14 Indels	cttcaagabarcaccagtgtttgatgababtgab 	GGGGAC 
	,×	; Len	PATGAA 	GTTTT         GTTTT
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5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		itch 148	п п	61
	ULT 1 09-801-876 equence 1, atent No. ENERAL INF APPLICANT: TITLE OF 1 TITLE	Query Ma Best Loc Matches		
	RESULT US-09- Seque Pate GENE TIT TIT TIT TIT TIT TIT TIT SEO SOO SOO SOO SOO US-09- OR	ÕĂÏ	8 8	දි අ

Db 1261 CTGACAGTAGCTCCTGC  Qy 1321 CAAAAAAGGCAGCACAA  Db 1321 CAAAAAAGGCAGCACACAA  Qy 1381 ACATCAATCAATCGTGTGT  Db 1381 ACATCAATCAATCGTGTGT  Qy 1441 TTTATCTAAAATGACAGAA  Db 1441 TTTATCTAAAATGACAGAAGAAA	RESULT 2 US-10-667-442-1 Sequence 1, Application US/10 PUDLICATION NO. US20040043466, GENERAL INFORMATION: APPLICANT: YE, Jane et al TITLE OF INVENTION: ISOLATED TITLE OF INVENTION: ACID MO TITLE OF INVENTION: THEREOF FILE REPERENCE: CLOOL160DIV CURRENT APPLICATION NUBER: CURRENT PILING DATE: 2003-0 NUMBER OF SEQ ID NOS: 8 SOPTWARE: FASTSEQ FOF WINDOM SEQ ID NO 1 LENGTH: 1485 TYPE: DNA ORGANISM: Homo sapiens US-10-667-442-1	Query Match Best Local Similarity 100.0 Matches 1485; Conservative  Qy   1 CCATGGGAGCGAACACT Db   1 CCATGGGAGCGAACACT  Qy   61 TTGACCACTTTGAAATT Db   61 TTGACCACTTTGAAATT  Qy   121 TACAGAAGAATGAAATGAAATGAAATGAAATGAAATGAA	Oy 181 TGGAGCGCAATGAAGTG Db 181 TGGAGCGCAATGAAGTG Oy 241 ACCCTTTCCTGGTTAAT Db 241 ACCCTTTCCTGGTTAAT Oy 301 TGGACCTCCTGGTTAAT Db 301 TGGACCTCCTGGGT Oy 361 AAGAACAGTGAAGCTC Oy 361 AAGAACAGTGAAGCTC Oy 421 AGCGCATCATTCACAGC Oy 421 AGCGCATCATTCACAGG Oy 421 AGCGCATCATTCACAGG Oy 421 AGCGCATCATTCACAGG Oy 481 TGCACATCACAGATTTCACAGG
		721 CGACTGTTGTAACTTACCCTTCTGCCTGGTCAACAGGAAATGGTCACTTCTTAAAAAGC 780 721 CGACTGTTGTAACTTACCCTTCTGCCTGGTCACAGGAAATGGTCACTTCTTAAAAAGC 780 721 CGACTGTTGTAACTTACCCTTCTGCCTGGTCACAGGAAATGGTCACTTCTTAAAAAGC 780 781 TACTCGAACCTAATCCAGACCAACGATTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840 781 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 840 841 ATATGAATGAATGAACTGGGATGTTTTCAGAAGAGGCTCATTCCAGGTTTCATTC 900 841 ATATGAATGAATGAATGAGATTTTTCAGAAGAGGCTCATTCCAGGTTTCATTC 900 841 ATATGAATGAATGAATTGTGAATTTTCAGAAGAGGCTCATTCCAGGTTTCATTC 900 901 CTAATAAAGGCAGGCTGAATTGTGAATCCTACCTTTGAACTTGAGGAAATGATTTTGGAGT 960 901 CTAATAAAAGGCAGGCTGAATTGTGAATCCTACCTTTCAACTAAGGAAATGATTTTGGAGT 960	961 CCAAACCTCTACATAAGAAAAAAAAGGCTCTGGCAAAGAAGGAAAGGATATGAGGAAAT 1020 961 CCAAACCTCTACATAAGAAAAAAAAGACGTCTGGCAAAGAAAG
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ACACAGTGAAGGGTCCTGGGCCTCAGCTCCTGGAAAGTCATTTC 1380
                                                                        STREATCTAGAGCAAGTCACTTAGCCACTTTCTGTGCTTTACTTTA 1440
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CCACTCCACACACCATGACTTAGAAAATGTGAATGAATATATTT 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 1485;
                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                0%; Score 1485; I
0%; Pred. No. 0;
0; Mismatches
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Gaps . 0 120

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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF PROTEINS, AND USES FILE REFERENCE: CLOO1160DIV CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 202-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGAAATTGTACACACGTTTGAGA 720
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                                                                                                                                                                                                                                                                            100.0%; Score 1485;
100.0%; Pred. No. 0;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 1485; Conservative
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; ORGANISM: Human
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Sequence 1, Application US/10254869
Publication No. US20030027307A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al

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is Sequence 100, Application US/10410764

is Publication No. US20040005664A1

is GENERAL INFORMATION:

is APPLICANT: Milennium Pharmaceuticals, Inc.

is APPLICANT: MacBeth, Kyle J.

is APPLICANT: MacBeth, Kyle J.

is APPLICANT: MacBeth, Kyle J.

is APPLICANT: Weich, Nadine S.

is APPLICANT: Weich, Nadine S.

is APPLICANT: Stai, Fong-Ying

is APPLICANT: Stai, Fong-Ying

is APPLICANT: Carroll, Joseph M.

is APPLICANT: Carroll, Joseph M.

is APPLICANT: Carroll, Joseph M.

is TITLE OF INVENTION: 58764, 62113, 33144, 32235, 23565, 13305, 14911, 86216, 171LE OF INVENTION: 58764, 62113, 3144, 32235, 23565, 13305, 14911, 86216, 171LE OF INVENTION: 58764, 62113, 3144, 32235, 23565, 13305, 14911, 86216, 171LE OF INVENTION: 5806 AND 8843 MOLECULES AND USES THEREFOR FILE REFERENCE: MPIOS-05-20MNIM

is CURRENT FILING DATE: 2001-04-10

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is PRIOR FILING DATE: 2000-09-01

is PRIOR FILING DATE: 2000-09-01

is PRIOR FILING DATE: 2000-09-01

is PRIOR FILING DATE: 2001-24
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347 TGGACCTCCTGCTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCACTTCAAGG
PRIOR APPLICATION NUMBER: US 60/351,572
PRIOR FILING DATE: 2002-01-24
PRIOR PLING DATE: 2001-09-7
PRIOR PLING DATE: 2001-09-7
PRIOR PLING DATE: 2001-09-7
PRIOR APPLICATION NUMBER: US 60/238,054
PRIOR APPLICATION NUMBER: US 60/238,054
PRIOR PLING DATE: 2000-10-05
PRIOR PLING DATE: 2001-10-29
PRIOR PLING DATE: 2001-10-29
PRIOR PLING DATE: 2001-10-29
PRIOR PLING DATE: 2001-20-29
PRIOR APPLICATION NUMBER: US 60/347,815
PRIOR PLING DATE: 2001-0-29
PRIOR PLING DATE: 2001-0-29
PRIOR PLING DATE: 2001-0-29
PRIOR PLING DATE: 2001-0-29
PRIOR PLING DATE: 2001-0-30
PRIOR PLING DATE: 2001-0-30
PRIOR PLING DATE: 2001-0-316
PRIOR PLING DATE: 2001-0-316
PRIOR PLING DATE: 2001-0-3-16
PRIOR APPLICATION NUMBER: US 60/269,440
PRIOR PLING DATE: 2001-0-3-16
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82.7%; Score 1228.6;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1231; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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; LOCATION: (49)
US-10-410-764-100
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LENGTH: 1281
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942 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGCAGGGT 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 1594;
                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040038881A1 7946584CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 1188.2;
99.7%; Pred. No. 0;
Live 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/232, 654
PRIOR FILING DATE: 2000-09-14
PRIOR PPLICATION NUMBER: US 60/234, 902
PRIOR PLLING DATE: 2000-09-22
PRIOR PLLING DATE: 2000-09-29
PRIOR PLLING DATE: 2000-09-29
PRIOR PLLING DATE: 2000-10-06
PRIOR PLLING DATE: 2000-10-06
PRIOR PLLING DATE: 2000-10-06
PRIOR PLLING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PERL PROGRAM
SEQ ID NO 44
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.7
Matches 1190; Conservative
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                                                 CGACTGTTGTAACTTACCCTTCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGC
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                            GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGA
                                                                                                                               767 CGACTGTTGTAACTTTACCCTTCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGC
                                                                                                                                                                                         TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT
                                                                                                                                                                                                                TACTCGAACCTAATCCAGACCAAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT
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TITLE OF INVENTION: HUWAN KINASES
FILE REFERENCE: PF-0209 USN
CURRENT FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-09-08
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Sequence 1, Application Wo. US20040048310A1

FUNDICATION NO. US20040048310A1

GENERAL INFORMATION:

APPLICANT: PLOWMAN, GREGORY D.

APPLICANT: WHYTE, DAVID

APPLICANT: WANNING, GERARD

APPLICANT: WANNING, SUCHA

TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE

TITLE OF INVENTION: BNZYMES

FILE REPRENCE: 038602/1366

CURRENT FILING DATE: 2001-07-07

PRIOR FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 1

LENGTH: 1594
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80.0%; Score 1188.2;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1190; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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162 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACC AGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACG 1002 ATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCC 1062 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGA CTAATAAAGGCAGGCTGAATTGTGATCCTACCTTTGAACTTGAGGAAATGATTTTGGAGT 1302 CTAATAAAGGCAGGCTGAATTGTGATCCTACCTTTGAACTTGAGGAAATGATTTTGGAGT GCGATTCTTCTCAGACATGTCTTCTAGAGCACCTTGACTCTGTCCAGAAGGAGTTCA 1422 GCGATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAGAAGAGTTCA 1081 TAATTITCAACAGAGAAAAGTAAACAGGGACTITAACAAAAGACAACCAAATCTAGCCT ACCCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCATGGTGG 601 ATTCCTTTGCTGTTGACTGGTGCTCCTGGGAGTGACGGCATATGAACTGCTGAGGGCC 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGA 841 ATATGAATGATATAAACTGGGATGCAGTTTTTCAGAAGAGGCTCATTCCAGGTTTCATTC TECACATCACAGATTTCAACATTGCTGCGATGCTGCCCAGGGAGACACAGATTACCACCA TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGCAGGCT TACTOGRACCTARTCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT 1141 TGGAACAAACCAAAGACCACAAGGTGAGGATGAGATAACAATAACAATAA 1193 

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NAME/KEY: misc feature

NOS20030207299A1 7946584CB1
US-10-288-798-44
                 GENERAL INFORMATION:
APPLICANT: BANDMAN, Olga; NGUYEN, Danniel B;
APPLICANT: WALIA, Narinder K: HAFALIA, April J.A.;
APPLICANT: WALIA, Narinder K: GANDHI, Ameena R:
APPLICANT: YAO, Monique G: GANDHI, Ameena R:
APPLICANT: PATTERSON, Chandra; YUE, Henry;
APPLICANT: BAUGHN, Maiagopal; DING, Li;
APPLICANT: BAUGHN, Maiagopal; DING, Li;
APPLICANT: THORNION, Michael; ELLIOTT, Vicki S:;
APPLICANT: LU, Yan; ISON, Craig H. Y. Tom;
APPLICANT: AZIMZAI, Yalda; BURRILL, John D;
APPLICANT: AZIMZAI, Yalda; BURRILL, John D;
APPLICANT: LU, PAUNG, Janice; TANG, Y. Tom;
APPLICANT: LU, PUNG, Janice; TANG, Y. Tom;
APPLICANT: AZIMZAI, Yalda; BURREN, Bridget A.;
APPLICANT: LU, PUNG, Janice; POLICER, Jennifer L.;
APPLICANT: TRANKUMAR, Jayalaxmi; WARREN, Bridget A.;
APPLICANT: TRANKUMAR: US 60/236,499
FRIOR PELICATION NUMBER: US 60/234,902
FRIOR APPLICATION NUMBER: US 60/234,902
FRIOR FILING DATE: 2000-09-29
FRIOR FILING DATE: 2000-09-29
FRIOR FILING DATE: 2000-09-29
FRIOR FILING DATE: 2000-09-14
FRIOR FILING DATE: 2000-09-08
FRIOR APPLICATION NUMBER: US 60/231,357
FRIOR APPLICATION NUMBER: US 60/231,357
FRIOR APPLICATION NUMBER: US 60/232,654
FRIOR APPLICATION NUMBER: US 60/232,654
FRIOR FILING DATE: 2000-09-08
FRIOR APPLICATION NUMBER: US 60/232,654
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  Publication No. US20030207299A1
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ORGANISM: Homo sapiens
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Sequence 10, Application US/09841683

Patent No. US20020081600A1

GRNERAL INFORMATION:

APPLICANT: Hu, Yi

APPLICANT: Nepomnichy, Boris

APPLICANT: Nepomnichy, Boris

APPLICANT: Scoville, John

APPLICANT: Scoville, John

APPLICANT: Scoville, John

APPLICANT: OF INVENTION: No. US20020081600Alel Human Kinase Proteins and Polynucleotides

FILE REFERENCE: LEX-0167-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1541
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                                                                                                       TGCACATCACAGATTTCAACATTGCTGCGGATGCTGCCCAGGGAGACACAGATTACCACCA
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                                                                           421 AGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACG
                                                                                                                                                                                  TGCACATCACAGATTTCAACATTGCTGCGATGCTGCCCAGGGAGACACAGATTACCACCA
                                                                                                                                                                                                                                                                                         TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGCAGGCT
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                                                                                                                                                                                                                                          Query Match 79.9%; Score 1186.2; Best Local Similarity 99.7%; Pred. No. 0; Matches 1188; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/841,683
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199,499
PRIOR PILING DATE: 2000-04-25
PRIOR PLILING DATE: 2000-05-01
NUMBER: US 60/201,227
NUMBER: OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 1191
                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-10
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| Publication No. USZ0040005664A1
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| Publication No. USZ0040005664A1
| CREMEAL IMPORATION: | Molech No. USZ0040005664A1
| CREMEAL IMPORATION: | Molech No. USZ0040005664A1
| APPLICANT: | Wolch No. USZ004005664A1
| APPLICANT: | Wolch No. USZ0040005664A1
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; TYPE: DNA
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US-09-841-683-12
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                                                                                         4; Indels
                                                                   DB 16;
                                                                Score 1184.6;
Pred. No. 0;
0; Mismatches
                                                                Query Match
Best Local Similarity 99.7%;
Matches 1187; Conservative
                               ; LOCATION: (1)...(1191)
US-10-410-764-102
ORGANISM: Homo
          FEATURE:
NAME/KEY: CDS
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Sequence 12 Application US/09841683

Sequence 12 Application US/09841683

Patent No. US20020081600A1

GENERAL INFORMATION:

APPLICANT: Hu, Yi

APPLICANT: Wepomnichy, Boris

APPLICANT: Wang, Xiaoming

APPLICANT: Scoville, John

APPLICANT: Walke, D. Wade

TILLE OF INVENTION: No. US20020081600Alel Human Kinase Proteins and Polynucleotides

TILLE OF INVENTION NUMBER: US/09/841,683

CURRENT APPLICATION NUMBER: US 60/199,499

PRIOR PILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 60/201,227

PRIOR PLING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 12

SEQ ID NO 12

SEQ ID NO 12

SEQ ID NO 12
            1020
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Best Local Similarity 98.8
Matches 1171; Conservative
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Score 1160.6;
Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 60/201,227
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 1224
                                                                                                                                    78.2%;
98.8%;
                                                                                                                                    Query Match
Best Local Similarity 98.8
Matches 1169; Conservative
                                                                                    t TYPE: DNA
COGANISM: homo sapiens
US-09-841-683-8
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Patent No. US20020081600A1

Patent No. US20020081600A1

APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
APPLICANT: Nepomnichy, Boris
APPLICANT: Nepomnichy, Gregory
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Scoville, Ush
APPLICANT: Scoville, Ush
APPLICANT: Walke, D. Wade
TITLE OF INVERTION: No. US20020081600Alel Human Kinase Proteins and Polynucleotides
TITLE OF INVERTION: NO. US20020081600Alel Human Kinase Proteins and Polynucleotides
CURRENT PILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199,499
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                                             0; Gaps
DB 9; Length 1224;
                                             14; Indels
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR PRILING DATE: 2000-04-27
PRIOR PAPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 239
LENGTH: 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 239, Application US/10276774; Publication No. US20040053245A1; GENERAL INFORMATION:
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US-10-276-774-239
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US-10-276-774-239
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Best Local Simi
Matches 674;
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ATGAATGATATAAACTGGGATGCAGTTTTTCAGAAGAGGCTCATTCCAGGTTTCATTCCT 900
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                                                GATTCTTCTCAGACATGTCTTCTAAGAGCACCTTGACTCTGTCCAGAAGGAGTTCATA
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Publication No. US20040005560A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATION: No. US20040005560A1e1 full length cDNA
FILE REPREBREE: 140106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT PELING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 231
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Best Local Similarity 99.4%;
Matches 1033; Conservative
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; ORGANISM: Homo sapiens
US-10-108-260A-231
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US-10-108-260A-231
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                             Length 711;
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                          Score 656.2; DB 9;
Pred. No. 1.3e-187;
0; Mismatches 3;
                          44.2%;
                          Query Match
Best Local Similarity 99.5
Matches 658; Conservative
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APPLICANT: Negomichy, Boris

APPLICANT: Nono, US20020081600Alel Human Kinase Proteins and Polynucleotides

FILE REPERENCE: LEX.0167-USA

CURRENT APPLICATION NUMBER: US 60/199, 499

PRIOR APPLICATION NUMBER: US 60/201, 227

PRIOR APPLICATION NUMBER: US 60/201, 227

PRIOR FILING DATE: 2000-04-25

SPRIOR FILING DATE: 2000-06-501

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO S

LENGTH: 71

TYPE: DNA

ORGANISM: homo sapiens
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                                                                                               ATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGCAGCTATTCCTTTGCTGTTGACTGG 620
                                                                                                                181 TGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCCGGAGACCGTATCATATTCGC 240
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61 ATTICTIGGATIGCTIGCTGCCCAGGAGACACAGATTACCACCATGGCTGGCACCAAGCCTTAC
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Sequence 4, Application US/09841683

Patent No. US20020081600A1

GENERAL INFORMATION:

APPLICANT: Hu, Yammichy, Boris

APPLICANT: Wang, Xiaoming

APPLICANT: Wang, Xiaoming

APPLICANT: Wang, Xiaoming

APPLICANT: Walke, D. Wade

TITLE OF INVENTION: No. US20020081600A1e1 Human Kinase Proteins and Polynucleotide:

TITLE OF INVENTION: No. US20020081600A1e1 Human Kinase Proteins and Polynucleotide:

FILE REFERENCE: LEX-0167-USA

CURRENT APPLICATION NUMBER: US/09/841,683

CURRENT PILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: US 60/199,499

PRIOR APPLICATION NUMBER: US 60/201,227
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; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 678
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-4
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Search completed: June 27, 2004, 00:23:55 Job time : 504 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-819-607-1

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Sequence 1, Application US/09801876B

Patent No. 6492155

GENERAL INFORMATION:

APPLICANT: WE Jane et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: 2001-09

CURRENT APPLICATION NUMBER: US/09/801,876B

CURRENT PILING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
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Sequence 2, Appli
Sequence 39, Appl
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 81, Appli
Sequence 81, Appli
Sequence 60, Appli
Sequence 61, Appli
Sequence 62, Appli
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Sequence 1298, Appli
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 0; Indels 0;
ALIGNMENTS
                              TYPE: DNA
CRGANISM: Human
US-09-801-876B-1
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TYPE: DNA
ORGANISM: Human
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Sequence 1, Application US/10254869
| Patent No. 663117
| Application US/10254869
| Patent No. 663117
| GENERAL INPORMATION:
| APPLICANT: YB, Jane et al APPLICANT: YB, Jane et al APPLICANT: YB, Jane et al ATID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF WINDER: US/10/254,869
| CURRENT APPLICATION UNDHER: US/10/254,869
| CURRENT FILING DATE: 2002-09-26
| NUMBER OF SEQ ID NOS: 8 | SOCTIONS | SEQ ID NOS: 8 | SEQ ID NOS: 8
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241 ACCCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCATGGTGG
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Pred. No. 0;
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
LENGTH: 1191
                                                                                                                                                                 79.9%;
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Best Local Similarity 99.7
Matches 1188; Conservative
                                                                                  TYPE: DNA
CORGANISM: homo sapiens
US-09-841-683-10
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Sequence 8, Application US/09841683
Patent No. 6617147
GENERAL INFORMATION:
APPLICANT: Walk, John
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: No. 661714761 Human Kinase Proteins and Polynucleotides Encodin FILE REFERENCE: LEX-0167-USA
CURRENT APPLICATION NUMBER: US/09/841,683
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APPLICANT: Nepomnichy, Boris
APPLICANT: Nepomnichy, Boris
APPLICANT: Neng, Xiaoming
APPLICANT: Donoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Conville, John
APPLICANT: Walke, D. Wade
TITLE REFERENCE: LEX-0167-USA
FILE REPERENCE: LEX-0167-USA
CURRENT APPLICATION NUMBER: US/09/841,683
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199,499
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
SPRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1675
                                                                         AAACCTCTACATAAGAAAAAAAAAGCGTCTGGCAAAGAAGGAGAAGGATATGAGGAAATGC 1020
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78.3%; Score 1162.6;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches
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Patent No. 6617147
GENERAL INFORMATION:
APPLICANT: Hu, YI
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CORGANISM: homo sapiens
US-09-841-683-12
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US-09-841-683-12
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CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION UNMERS: US 60/199,499
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 8
TYPE: DNA
                                                                                                                     ; ORGANISM: homo sapiens
US-09-841-683-8
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Sequence 6, Application US/09841683

Sequence 6, Application US/09841683

Patent No. 6617147

GENERAL INFORMATION:

APPLICANT: Hu, Yi

APPLICANT: Wang, Xiaoming

APPLICANT: Donoblo, Gregory

APPLICANT: Walke, D. Wade

TITLE OF INVENTION: No. 6617147e1 Human Kinase Proteins and Polynucleotides Encodin

APPLICANT: Walke, D. Wade

TITLE OF INVENTION: No. 6617147e1 Human Kinase Proteins and Polynucleotides Encodin

SPLICE REPRENEE: LEX-0167-USA

CURRENT APPLICATION NUMBER: US 60/199,499

PRIOR PRING DATE: 2000-04-25

PRIOR PRING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

LEMENT FILING DATE: 2000-05-01

NUMBER OF SEX ID NOS: 12

SEQ ID NO 6

LEMENT FILING DATE: 2000-05-01

NUMBER OF SEX ID NOS: 12

SEX ID NO 6

LEMENT FILING DATE: 2000-05-01

NUMBER OF SEX ID NOS: 12
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        GAGCGCAATGAAGTAGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGCAC
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                                841 ATGAATGATATAAACTGGGATGCAGTTTTTCAGAAGAGGCTCATTCCAGGTTTCATTCCT
                                                                                                                                                       961 AAACCTCTACATAAGAAAAAAAGGTCTGGCAAAGAAGAAGAAGAATATGAGGAAAATGC
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843 ATGAATGATATAAACTGGGATGCAGTTTTTCAGAAGAGGCTCATTCCAGGTTTCATTCCT
                                                                                                                            AATAAAGGCAGGCTGAATTGTGATCCTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC
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    121 CAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAAAGTGCGTG 180
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                                                                       GAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACTCCCAGATCATGCAGGGGTCTGGAGCAC
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Pacent No. 6638721

GENERAL INFORMATION:
APPLICANT: Mayers, Rachel
APPLICANT: Malliamanon, Mark
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
TITLE OF INVENTION WUMBER: 05/09/79,875
CURRENT APPLICATION WUMBER: 06/182,059
FRIOR APPLICATION WUMBER: 06/182,059
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION WUMBER: 09/659,287
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION WUMBER: 09/659,287

NUMBER OF SEQ ID NOS: 32

SOPTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 15:
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Best Local Similarity 66.5%; Pred. No. 9.2e-142;
Matches 726; Conservative 0; Mismatches 354;
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CORGANISM: Homo sapiens
US-09-799-875-15
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APPLICANT: Hu, Yi

APPLICANT: Nepomnichy, Boris

APPLICANT: Wang, Xiaoming

APPLICANT: Wang, Xiaoming

APPLICANT: Scorille, John

APPLICANT: Scorille, John

APPLICANT: Scorille, John

APPLICANT: Walke, D. Wade

ITILE OF INVENTION: No. 6617147el Human Kinase Proteins and Polymucleotides Encoding

ITILE OF INVENTION: No. 6617147el Human Kinase Proteins and Polymucleotides Encoding

ITILE OF INVENTION: NO. 6617147el Human Kinase Proteins and Polymucleotides Encoding

CURRENT APPLICATION NUMBER: US/09/841,683

CURRENT FILING DATE: 2000-04-24

PRIOR PILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 60/199,499

PRIOR APPLICATION NUMBER: US 60/201,227

PRIOR PILING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 678
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                                                                                             301 GACCTCCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCACTCAAGGAA 360
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                                                                    GACCTCCTGCTGGGTGGAGCCTGCGTTATCACCTGCAACAGAACGTCCACTTCAAGGAA 362
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Patent No. 6617147
GENERAL INFORMATION:
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ORGANISM: homo sapiens
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Sequence 13, Application US/09799875 Patent No. 6638721 GENERAL INFORMATION:

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                                           APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Mark
TITLE OF INVENTION: No. 6538721el Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: 35800/20996
CURRENT APPLICATION NUMBER: 08/09/799,875
CURRENT FILING DATE: 2010-03-06
PRIOR APPLICATION NUMBER: 60/182,059
PRIOR PLING DATE: 2000-09-11
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1826
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Best Local Similarity 66.5%; Pred. No. 1.2e-141;
Matches 726; Conservative 0; Mismatches 354;
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Meyers, Rachel
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; NAME/KEY: CDS
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US-09-799-875-13
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Sequence 3, Application US/09801876B
Patent No. 6492155
Patent No. 6492155
GRENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OP INVENTION: THEREOF
TITLE OP INVENTION: THEREOF
FILE REFERENCE: CLOO1160
CURRENT APPLICATION NUMBER: US/09/801,876B
CURRENT PILING DATE: 2001-03-09
NUMBER OP SEQ ID NOS: 8
SOFTWARE: FRRESEQ for Windows Version 4.0
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US-09-801-876B-3
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Patent No. 6686176

GENERAL INFORMATION:
GENERAL INFORMATION:
TATLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE OF INVENTION: THEREOF FILE OF INVENTION: NUMBER: US/09/819,607

CURRENT PAPLICATION NUMBER: US/09/819,607

CURRENT PILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FeatSEQ for Windows Version 4.0

SEQ ID NO 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1073 GACTATCTTCAAGACTGCCTCGATGCCATCCAGCAAGACTTCGTGATTTTTAACAGAGAA 1132
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   113 AGCAACGCCGTGGAGTCCCTGGTGCAGCTGTTCAGCACCGTGAGCGTCCAGTATGTCCCC 772
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                                                                                                                  773 ACGIGGICCAAGGAGATGGIGGCTIGCGGAAGCICCTCACIGIGAACCCCGAGGAC
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                                                                            744 GCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGCTACTCGAACCTAATCCAGACCAA
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31.4%; Score 466.8; DB 4; Length 1
Best Local Similarity 65.9%; Pred. No. 5.9e-137;
Matches 713; Conservative 0; Mismatches 357; Indels
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ORGANISM: Human
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US-09-819-607-1
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US-09-819-607-1
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Sequence 3, Application US/09394455

Sequence 3, Application US/09394455

Batent No. 6531305

GENERAL INFORMATION:

APPLICANT: Witman, George F.

APPLICANT: George F.

APPLICANT: George F.

TITLE OF INVENTION: SPERM ASSOCIATED PROTRIN KINASE POLYPEPTIDES, CORRESPONDING:

TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE

TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE

FILE REPERENCE: 07917/078001

CURRENT APPLICATION NUMBER: US 60/099,771

PRIOR FILING DATE: 1998-09-10

PRIOR FILING DATE: 1998-09-10

NUMBER OF SEQ ID NOS: S6

SOFTWARE: FBESEG FOR Windows Version 4.0

SEQ ID NO 3

LENGTH: 1008
                                                                                                                                                                                                                             146378 CCACTCCACCACCATGACTTAGAAATGTGAATGAATATATTTTCAAAAAGGCAGCACA 146437
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                                                                                                                                             146318 ACAATCTCATGCCAGAAACTTCTAATTACATATGTCAAGAAAAGCTGACAGTAGTTCTTG
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                                                                   146258 CCCACAAGGTGAGGATGGTCAGAATAACAACTTGTAAAGGCCTCATGTCTTCTTCTGGG
                                                                                                                   1217 ACAATCTCATGCCAGAAACTTCTAATTACATATGTCAAGAAAAGCTGACAGTAGCTCCTG
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8.9%; Score 132.6; DB 4; Length:
Best Local Similarity 54.1%; Pred. No. 2e-31;
Matches 323; Conservative 0; Mismatches 259; Indels
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ORGANISM: Homo sapiens
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; LOCATION: (1)...(1008)
US-09-394-455-3
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US-09-394-455-3
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US-10-254-869-3
; Sequence 3, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
; TITLE OF INVENTION: THEREOF
; FILE REPERENCE: CL001166DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PRESEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 148567
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                                                                                                                                                                                           Query Match 24.5%; Score 363.4; DB 4; Length 148567; Best Local Similarity 98.4%; Pred. No. 7.6e-103; Matches 367; Conservative 0; Mismatches 6; Indels 0;
                 | LENGTH: 148567
| TYPE: DNA
| ORGANISM: Human
| FEATURE:
| JACKTION: (1) ... (148567)
| OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(148567); OTHER INFORMATION: n = A,T,C or GUS-10-254-869-3
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ORGANISM: Human
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SEQ ID NO 3
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Sequence 5, Application US/09394455
Patent No. 6531305
GENERAL INFORMATION:
APPLICANT: Witman, George F.
APPLICANT: Mitman, George F.
APPLICANT: Leszyk, John D.
APPLICANT: Leszyk, John D.
TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE FILE REPRENCE: 07911/07801
CURRENT APPLICATION NUMBER: US/0394,455
CURRENT APPLICATION NUMBER: US 60/099,771
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FRAESEQ for Windows Version 4.0
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414 CAGAACCAGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACAT 473
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8.9%; Score 132.6; DB 4;
Best Local Similarity 54.1%; Pred. No. 4e-31;
Matches 323; Conservative 0; Mismatches 259;
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LOCATION: (81)...(1133)
NAME/KEY: misc_feature
LOCATION: (1)...(2549)
OTHER INFORMATION: n = A,T,C or G
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LENGTH: 2549
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GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Coweert
APPLICANT: Lex M. Coweert
TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION
FILE REFERENCE: RTS-0088
CURRENT PALLICATION UNDERR: US/09/467,082
CURRENT PALLING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 49
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                                  ATGGTGGTGGACCTCCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCAC 353
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Best Local Similarity 54.1%; Pred. No. 4e-31;
Matches 323; Conservative 0; Mismatches 259; Indels
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COTHER INFORMATION: unknown
US-09-467-082-3
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ORGANISM: Homo sapiens
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NAME/KEY: CDS
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QQ	495 TTCAG	TICAGTGAGCCCCATGCCCGTTTCTACGCGGCCCAGATCGTCCTGACTTTGAGTATCTG 554	
ò	414 CAGAA	414 CAGAACCAGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACAT 473	
qq	555 CACTO	555 CACTCGCTGGATCTCTACAGGGACCTGAAGCCGGAGAATCTGCTCATTGACCAGCAG 614	
È	474 GGGCA	474 GGGCACGTGCACATCACAGATTTCAACATTGCTGCGATGCTGCCCAGGGAGACACAGATT 533	
QQ	615 GGCTA	615 GGCTACATTCAGGTGACAGACTTCGCCAAGCGCGTGAAGGGCCGCACT 668	
È	534 ACCAC	534 ACCACCATGGCACCAAGGCCTTACATGGCACCTGAGATGTTCAGGTCCAGAAAAGGA 593	
q	669 TGGAC	669 TGGACCTTGTGGGGCCCCTGAGTACCTGGGCCCCTGAGTTATCCTGAGCAA 721	
è	594 GCAGG	GCAGGCTATTCCTTTGCTGTTGACTGGTGGTCCTGGGAGTGACGGCATATGAACTG 650	
qq	722AGG	722AGGCTACAACAGGCGTGGACTGGTGGGCCCTGGGGGTTCTTATCTATGAAATG 776	
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genesequ2001bs:\*
genesequ2002s:\*
genesequ2003bs:\*
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genesequ2004s:\*

Description	Abs55499 cDNA enco	Aca62840 cDNA enco	Aai70704 Human 149	Aah46891 cDNA enco	Aad34317 Human PKI	Aad23679 Novel hum	Aad23680 Novel hum	Aad23678 Novel hum	Aas06704 Polynucle		Aad23677 Novel hum	Aad23676 Novel hum	Abg61051 Serine/th	Novel	Ada19317 Human ins	Acc72764 Human can	Ade38374 Human pro	Aas46210 Human DNA	~	Aca75785 Novel hum	Aca71265 Human sec	Acc87793 Human sec	Acc87179 Human sec
SUMMARIES	ABS55499	ACA62840	AAI70704	AAH46891	AAD34317	AAD23679	AAD23680	AAD23678	AAS06704	ABA08463	AAD23677	AAD23676	ABQ61051	AAF44625	ADA19317	ACC72764	ADE38374	AAS46210	ABX78813	ACA75785	ACA71265	ACC87793	ACC87179
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% Query Match	100.0	100.0	82.7	80.0	80.0	79.9	78.3	78.2	56.0	45.3	44.2	44.1	36.4	36.4	36.4	36.4	36.4	34.8		34.8	34.8	34.8	34.8
Score	1485	1485	1228.6	1188.2	1188.2	1186.2	1162.6	1160.6	831.2	672.8	656.2	655.2	540.8	540.8	540.8	540.8	540.8	516.4	516.4	516.4	516.4	516.4	516.4
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The present invention relates to the isolation of a human kinase and the polymucleotide sequences encoding it. The human kinase of the invention is related to the serine/threonine kinase subsamily. The gene encoding the human kinase subsamily. The gene encoding the human kinase is located on chromosome 5. The polymedide and disease or condition mediated by a human kinase. Both the polypeptide and polymucleotide sequences of the invention are useful for treating a disease or condition mediated by a human kinase. Both the polypeptide and polymucleotide sequences are useful as models for the development of human therapeutic agents, and as query sequences to development of human therapeutic agents, and as query sequences to perform a search against sequence date bases to identify other family members of related sequences. The polympeptide is useful to raise antibodise or to elicit another immune response, as a resident in seasys antibodise or to elicit another immune levels of the protein in biological fluids, as markers for tissues in which the corresponding protein is sepected to protein in its natural state.

CC designed to quantitatively determine levels of the protein in biological fluids, as markers for tissues in which the corresponding protein in the natural state, or an altered form that causes the specific disease or pathology associated with the kinase, to screen a compound for the ability to stimulate or inhibit interaction between the kinase protein, and in pharmacogenomic analysis. The polymucleotide is useful for a crivity of the human kinase gene in clinical trials or in a treatment regimen, in diagnostic assays for qualitative changes in a human kinase constructs to control human kinase gene expression, and to produce transgenic animals. The present sequence expression, and to produce transgenic animals. The present sequence containing cells a human kinase related to the serine/threamily.

Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other; 

ö 300 480 TGGAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGC 240 241 ACCCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCATGGTGG 300 301 · TGGACCTCCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGGAACGTCCACTTCAAGG 360 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACC 420 61 TTGACCACTTTGAAATTTTGCGAGCCATTGGGAAAGGCAGTTTTGGGGAGGTCTGCATTG 120 TACAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAAAGTGCG 180 181 TGGAGCGCAATGAAGTGAAAATGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGC 240 301 TGGACCTCCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCACTTCAAGG 360 CCATGGGAGCGAACACTTCAAGAAAACCACCAGTGTTTGATGAAAATGAAGATGTCAACT 60 AGGGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACG AGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACG 61 TIGACCACTITICAAAITITIGCGAGCCATIGGGAAAGGCAGTITITIGGGGAGGTCTGCATIG 121 TACAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAAAGTGCG ACCCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCATGGTGG CCATGGGAGCGAACACTTCAAGAAAACCACCAGTGTTTGATGAAAATGAAGATGTCAACT Gaps o; DB 7; Length 1485; 0; Indels 100.0%; Score 1485; 1 100.0%; Pred. No. 0; tive 0; Mismatches Query Match Best Local Similarity 100. Matches 1485; Conservative 181 361 421 241 8 g ઠે 셤 ò g 셤 요 a ò 셤 ક 8 8

1080 1080 1200 1200 1260 1260 1380 1380 1020 1020 1381 ACATCAATCAACTGTGTGTGTGAGGAAGTCACTTAGCCACTTTCTGTGTTTTACTTTA 1440 99 660 720 720 780 780 840 840 900 900 960 960 600 9 961 CCAAACCTCTACATAAGAAAAAAAGCGTCTGGCAAAGAAGAAGAAGGATATGAGGAAAT 1021 GCGATTCTTCTCAGACATGTCTTCTTCAGAGCACCTTGACTCTGTCCAGAAGGAGTTCA ATGICITCITCITGGGACAATCICATGCCAGAAACTICTAATTACATATGICAAGAAAG ATGTCTTCTTGGGACAATCTCATGCCAGAAACTTCTAATTACATATGTCAAGAAAAG CAAAAAGGCAGCACAACACAGTGAAGGGTCCTGGGCCTCGAGGCCTCGAAAGTCATTTC ATATGAATGATATAAACTGGGATGCAGTTTTTCAGAAGAGGCTCATTCCAGGTTTCATTC 961 CCAAACCTCTACATAAGAAAAAAAGGTCTGGCAAAGAAGGAGGAAGATATGAGGAAAT 1081 TAATITICAACAGAGAAAAGTAAACAGGGACTTTAACAAAAGACAACCAAATCTAGCCT TGGAACAAACCAAAGACCCACAAGGTGAGGATGGTCAGAATAACAACTTGTAAAGGCCTC CIGACAGIAGCICCIGCCACTCCACACACAIGACTIAGAAAAIGIGAAIGAATAIATIT ACATCAATCAACTGTGTGATCTAGAGCAAGTCACTTAGCCACTTTCTGTGCTTTACTTTA 481 TGCACATCACAGATTTCAACATTGCTGCGATGCTGCCCAGGGAGACACAGATTACCACCA 661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGA 721 ceacherrarachtracchrichechesteacadaaaresteachtraraaaaec CAAAAAAGGCAGCACAACACAGTGAAGGGTCCTGGGCCTGAGCTCCTGGAAAGTCATTTC 601 ATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCC 601 ATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCC CTAATAAAGGCAGGCTGAATTGTGATCCTACCTTTGAACTTGAGGAAATGATTTTGGAGT 1021 GCGATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAGGAGTTCA TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGCAGGCT CGACTGTTGTAACTTACCCTTCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGC TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT ACA62840 standard; cDNA; 1485 901 1141 1201 1201 1261 1321 1321 1381 1441 1261 541 781 841 661 721 ACA62840 ID ACA6 XX RESULT 2 g 음 ሯ 셤 ò 셤 à 요 ઠે 셤 ठे 셤 ઠ 셤 ò 셤 ò 셤 셤 ò 셤 셤 ઠ 유 ò ò 셤 8 ò ò ઠે

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                                                                                                             ACCCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCATGGTGG
                                                                                                                                                                                                                        TGGACCTCCTGCTGGGTGGAGACCTGCCTTGCAACAGAACGTCCACTTCAAGG
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                                                               cDNA encoding human kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                               colon cancer;
             CAAAAAAGGCACACAACACAGTGAAGGGTCCTGGGCCTGAGCTCCTGGAAAGTCATTTC
                                                                                                                                CAAAAAAGGCAGCACACACACAGTGAAGGGTCCTGGGCCTGAGGCTCCTGGAAAGTCATTTC
                                                       CTGACAGTAGCTCCTGCCACTCCACACACCATGACTTAGAAAATGTGAATGTATTTT
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                                                                                                                                                                                                                             Protein kinase; human; signal transduction; lung cancer; brain cancer; breast cancer; gene therapy; diagnosis; ss.
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15-JUN-2000; 2000US-00593927.
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P-PSDB; AAM50334.
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lung cancer (claimed), and methods for evaluating the efficacy of treatment. 14911 nucleic acids are useful in diagnostic, screening and gene therapy methods, for recombinant protein production, in the design of probes and primers, as a pharmacogenomics marker, and in the breeding of transgenic animals in which a 14911 gene is introduced or disrupted. Antisense 14911 and ribozyme molecules are used in a claimed method of treating cancer or a cellular proliferation and/or differentiation disorder. In addition to cancer, such disorders include those associated with bone metabolism, autoimume diseases, cardiovascular disorders, liver disorders, viral diseases, pain and metabolic disorders,
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                                                                                                                                                                                                                                                      Query Match 82.7%; Score 1228.6; DB 6; Length 1281; Best Local Similarity 99.7%; Pred. No. 0; Masmatches 1231; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                   Sequence 1281 BP; 392 A; 277 C; 299 G; 313 T; 0 U; 0 Other;
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                                                                                                                                                                   GCGATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAGGAGTTCA
                                                                                                                                                                                  1067 GCGATTCTTCTCAGACATGTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAAGGAGTTCA
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                ATATGAATGATAAACTGGGATGCAGTTTTTTCAGAAGAGGCTCATTCCAGGTTTCATTC
                                                                              947 CTAATAAAGGCAGGCTGAATTGTGATCCTACCTTTGAACTTGAAGAAATGATTTTGGAGT
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404. .1594
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31-JAN-2000; 2000US-0179364P.
17-FEB-2000; 2000US-0183173P.
17-MAR-2000; 2000US-0190162P.
29-MAR-2000; 2000US-0193404P.
13-NOV-2000; 2000US-0247013P.
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                                                                                                                                                                                                                                                                                                               dementia, manic depression, etc. The polynucleotides are useful in gene
therapy techniques to treat the above mentioned disorders. Sequences
AAH46891-46922 represent human protein kinases encoding cDNA molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          642 ACCCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAAGAAGAAAATGTTCATGGTGG
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viral infections, diabetes, obesity, organ transplant rejection and
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.0%; Score 1188.2; DB 4; Length 1594; Best Local Similarity 99.7%; Pred. No. 0; Matches 1190; Conservative 0; Mismatches 3; Indels 0;
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                                    Example 1, Page 201; 218pp; English
              rheumatoid arthritis.
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TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGCAGGCT 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGATTCTTCTCAGACATGTCTTCTAGAGCACCTTGACTCTGTCCAGAAGGAGTTCA
                                                                                          GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGA
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                                                 1002 ATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCC
                                                                                                                          GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGA
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                                                                                                                                                       CGACTGTTGTAACTTACCCTTCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGC
                                                                                                                                                                                                                      TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT
                               601 ATTCCTTTGCTGTTGACTGGTGGTCCTGGGAGTGACGCCATATGAACTGCTGAGAGGCC
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/product= "Human PKIN-20 protein"
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The present invention relates to human kinases (PKIN) and polynucleotides encoding such proteins. PKIN sequences of the invention are useful for disponeing, treating or preventing disorders associated with aberrant expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS) thymic hypoplasia, Crohn's disease, ansemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-Tooth disease or seizures), cell proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma), and developmental disorders (e.g. bown's syndrome). They are also used in human PKIN-20 protein therapy. The present sequence is a cDNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 1188.2; DB 6; Length 1594; 99.7%; Pred. No. 0;
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0; Mismatches
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                         08-SEP-2000; 2000US-0231357P.
14-SEP-2000; 2000US-0231557P.
22-SEP-2000; 2000US-0234902P.
06-OCT-2000; 2000US-0236499P.
13-OCT-2000; 2000US-0238389P.
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P-PSDB; AAE21725.
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                                                                                                                                  1002 AFTCCFFFGCTGFFGACTGGTGGTCCCTGGGAGTGACGGCAFATGAACTGCTGAGAGGCC 1061
                                                                                                                                                                                                                                                                                                 1242 ATATGAATGATATAAACTGGGATGCAGTTTTTCAGAAGAGGCTCATTCCAGGTTTCATTC 1301
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                                                                                           1062 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAATTGTACACACGTTTGAGA 1121
                                                                                                                                                                                                                         1122 cdactigitigiaactitacccricigccrigitacadagaaatiggigicacticritaaaaagc 1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human protein; NHP; gene therapy; diagnosis; drug screening; gene expression; bresst cancer; prostate cancer; nutriceutical; cosmetic; medical disorder; mental; biological; physiological; chemotherapeutic;
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                                                 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGCAGGCT 600
                    881
          1182 TACTCGAACCTAATCCAGACCAACGATTTCTCAGTTATCTGATGTCCAGAACTTCCCGGT
                                                                                                                                                                                                                                                                                                                                          1021 GCGATTCTCTCAGACATGTCTTCTAAGAGCACCTTGACTCTGTCCAGAAGGAGTTCA
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                                      TGCACATCACAGATTTCAACATTGCTGCGATGCTGCCCAGGGAGACACAGATTACCACCA
                                                                                                                                                              GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGA
                                                                                                                                                                                                    CGACTGTTGTAACTTACCCTTCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGC
                                                                                                                                                                                                                                             781 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT
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The invention relates to novel human protein (MHP) kinases and their corresponding cDNA molecules. MHP kinase and its DNA are useful as cagents in assays for screening compounds that can be used as the content of mental, plantacettical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and treatment of physiological disorders or diseases, and cosmetic and the mapping of a unique gene to a particular chromosome. MHP DNA is further useful as hybridisation probes for chromosome. MHP DNA is further useful as hybridisation probes for the detection of mutant NHPs or inappropriately expressed NHPs for disease diagnosis. NHP DNA is also useful in gene therapy. The present constituent protein kinases, thosomal protein kinases and camper. The dependent kinases cDNA related to the invention
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/product= "Novel human protein (NHP) kinase"
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79.9%; Score 1186.2; DB 6; Length
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1188; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoville J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Donoho
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                                                                                                                                                                                                                                                                                                       25-APR-2000; 2000US-0199499P.
01-MAY-2000; 2000US-0201227P.
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                                                                                                                                                                                                                                                                                                                                                                                                                             (LEXI-) LEXICON GENETICS INC
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                           GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACCAG
                                                                          CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACGTG
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Novel human protein; NHP; gene therapy; diagnosis; drug screening; gene expression; breast cancer; prostate cancer; nutriceutical; cosmetic; medical disorder; mental; biological; physiological; chemotherapeutic;
                                                                                                                                                                      Novel human protein (NHP) kinase full-length ORF and flanking region DNA.
                                                                                            AAD23680 standard; DNA; 1675 BP
                                                                                                                                               (first entry)
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421 AGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACG 480

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The invention relates to novel human protein (MHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as tharmaceutical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. MHP DNA is useful for disgnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and nutriceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as physiological diseases and also for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPs or inappropriately expressed NHPs for disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase full-length ORP (Open reading frame) and flanking region DNA related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 CCATGGGAGCCAACACTTCAAGAAAACCACCAGTGTTTGATGAAAATGAAGATGTCAACT
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                                                                                                                                                                                                                                         Wang X, Donoho G, Scoville J, Walke DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 78.3%; Score 1162.6; DB 6; Length 1675; Best Local Similarity 98.8%; Pred. No. 6.7e-312; Matches 1171; Conservative 0; Mismatches 14; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 44; 44pp; English.
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01-MAY-2000; 2000US-0201227P.
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                831 AGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACG
                                                                1011 ATTCCTTTGCTGTTGACTGGTGCTCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCC
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                                                                                                           TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGCAGGCT
                                                                                                                                                                        ATTICCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCC
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                                              TGCACATCACAGATTTCAACATTGCTGCGATGCTGCCCAGGGAGACACAGATTACCACCA
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TGGAACAAACCAAAGACCCACAAGGTGAGGATGGTCAGAATAACA 1185
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1. .1224
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/\*tag= a /product= "Novel human protein (NHP) kinase"

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The invention relates to novel human protein (MHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as pharmaceutical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents cuseful in the treatment of breast cancer and prostate cancer. NHP DNA is useful in the treatment of breast cancer and prostate cancer. NHP DNA is cuseful in the treatment of breast cancer and prostate cancer. NHP DNA is creatment of physiological disorders or disasses, and cosmetic and custicular conformage and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for chromosome. NHP DNA is further useful as hybridisation probes for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPs or inappropriately expressed NHPs for General disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase cDNA which is similar to sequence is novel human protein (shownal protein kinases and cAMP-condependent kinases cDNA related to the invention
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                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecules encoding new human proteins, useful in diagnosis, drug screening, clinical trial monitoring, treatment of
                                                                                                                                                                                                                                             Walke DW;
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78.2%; Score 1160.6; DB 6; Length 1224;
Best Local Similarity 98.8%; Pred. No. 2.1e-311;
Matches 1169; Conservative 0; Mismatches 14; Indels 0;
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                                                                                                                                                                                                                                             Donoho G, Scoville J,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 41; 44pp; English.
                                                                                                                                                                                                                                             Wang X,
                                                                                                   24-APR-2001; 2001WO-US013149
                                                                                                                                         25-APR-2000; 2000US-0199499P.
01-MAY-2000; 2000US-0201227P.
                                                                                                                                                                                                    (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                                                             Hu Y, Nepomnichy B,
                                                                                                                                                                                                                                                                                      WPI; 2002-034442/04.
P-PSDB; AAE14260.
                     WO200181557-A2.
                                                          01-NOV-2001
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Martinez R;

Sudarsanam S,

Manning G,

Whyte D, Clary D;

Plowman GD, Flanagan P,

22-NOV-2000; 2000WO-US032085.

99US-0167482P

24-NOV-1999;

(SUGE-) SUGEN INC.

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ATTTTCAACAGAGAAAAAGTAAAACAGGGACTTTAACAAAAGACAACCAAATCTAGCCTTG 1140
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361 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACCAG 420
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                                                                                              CACATCACAGATTTCAACATTGCTGCGATGCTGCCCAGGGAGACACAGATTACCACGTG
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protein kinases have been identified manipulation of the tyrosine or serine/threonine kinases (FTK and STK) families. The polynucleotides enconcing protein kinases and the polymptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoletic origin), cardiovascular cancers (especially cancers of haematopoletic origin), cardiovascular cancers (especially cancers of haematopoletic origin), cardiovascular cancers (especially cancers of haematopoletic origin), neurological immune related diseases (e.g. rheumatoid arthritis), neurological cancers (e.g. schizophremia), neurodegenerative disorders (e.g. disorders), parkinson's disease (e.g. rheumatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility).

Additionally, polymucleotides encoding protein kinases may be used for gene therapy and as DNA probes in disquostic assays. The protein kinase polypoptides may be used as antigens in the production of anthodies against the protein kinases and in assays to identify modulators of
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                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GACCACTTTGAAATTTTGCGAGCCATTGGGAAAGGCAGTTTTGGGGAGGTCTGCATTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAAAGTGCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.0%; Score 831.2; DB 4; 90.7%; Pred. No. 5.2e-220; iive 0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase expression and activity
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Best Local Similarity 90.7
Matches 903, Conservative
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; proliferation; metastasis; cancer; tumour; proliferation; athma, arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; ell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cyrostatic; osteopathic; vasculoric; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
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                                                                                                                                                                      GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGGAGGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                   723 ACTGTTGTAACTTACCCTTCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGCTA
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                                      421 CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACGTG
                                                                                                                                                                                                                                 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGAGGCCGG
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA0574 represent mucleic caids encoding them. The sequences ABA08225-ABA0574 represent mucleic caids encoding them. The currention also relates to vectors and recombinant host calls comprising a mucleotide of the invention. The producing the novel polypeptides of the invention. Although novel, many of the note polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence to polypeptides of the invention by the polypeptides of the invention may differential therapeutic applications. The polypeptides of the invention activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell ferentiation activities, including cytokine, cell proliferation or chemokinetic activities; haemostatic, thromoculatory activity, issue growth activity; compacted activities; haemostatic or chemokinetic activities; haemostatic, thromoculatory activities; haemostatic, thromoculatory activities; preventing, treating or amalorating may be useful for preventing, treating or amalorating medical activities; preventing them may be used to promote wound the invention are useful for preventing, treating or amalorating medical accivities and proliferative returnopathy, atherosclarosis, coronary heart disease, proliferative returnopathy, atherosclarosis, coronary heart disease, arterial inchaemia, bone disorders (e.g., myeloid or lymphoid cell growth. Polypeptides and ulcers), while those whum healing (e.g., of burns, incisions and ulcers), while those which activities and publy peused in the treatment of viral, bacterial and fungal infections in addition to immune disorders energates or accidental damage. The polypeptides may be used in the dam
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                                                                                                                                                                                                                                   Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
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45.3%; Score 672.8; DB 4; Length 678;
Best Local Similarity 99.7%; Pred. No. 4.1e-176;
Matches 674; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 678 BP; 203 A; 148 C; 152 G; 175 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 422; 1963pp; English.
03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                                                                                                              WPI; 2001-457740/49.
P-PSDB; ABB11219.
                                                                     (HYSE-) HYSEQ INC.
                                                                                                                 Tang YT, Liu C,
                                                                                                                                                                                                                                                                                     and cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression; breast cancer; prostate cancer; nutriceutical; cosmetic; medical disorder; mental; biological; physiological; chemotherapeutic;
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                                                                                                                                                                                                                                                                                                                     CTTCTTCAAGAGCACCTTGACTCTGTCCAGAAGGAGTTCATAATTATCAACAGAGAAAAA 660
                                                                                            TCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGCTACTCGAACCTAATCCAGAC 360
                                                                                                                                      TGTGATCCTACCTTTGAACTTGAGGAAATGATTTTGGAGTCCAAACCTCTACATAAGAAA 980
                                                       300
                                                                             TCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGCTACTCGAACCTAATCCAGAC 800
                                                                                                                                                                    541 AAAAAGCGTCTGGCAAAGAAGAAGAAGAATATGAGGAAATGCGATTCTTCTCAGACATGT
TCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGACGACTGTTGTAACTTACCCT
                                               TCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGACGACTGTTGTAACTTACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human protein; NHP; gene therapy; diagnosis; drug screening;
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/product= "Novel human protein (NHP) kinase"
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01-MAY-2000; 2000US-0201227P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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P-PSDB; AAB14259.
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The invention relates to novel human protein (MHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as cagents in assays for screening compounds that can be used as to pharmaceutical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents cuseful in the treatment of breast cancer and prostate cancer. NHP DNA is useful in the treatment of breast cancer and prostate cancer. NHP DNA is cuseful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and committee of coding sequence and the mapping of a unique gene to a particular of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPs or inappropriately expressed NHPs for disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase cDNA which is similar to serine/threonine protein kinases, cDNA related to the invention
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44.2%; Score 656.2; DB 6;
Best Local Similarity 99.5%; Pred. No. 1.7e-171;
Matches 658; Conservative 0; Mismatches 3;
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The invention relates to novel human protein (NHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as pharmaceutical reagents useful in the threatent of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and utriceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for creening libraries and assessing gene expression patterns, and also for the detection of mutant NHPB or inappropriately expressed NHPB for disease diagnosis. NHP DNA is also useful in gene therapy. The present engagenes is novel human protein (NHP) kinase CDNA which is similar to sequence is novel human protein (NHP) kinase CDNA which is similar to
                                                                                                                                                                                                                                                                                                       Novel human protein, NHP; gene therapy; diagnosis; drug screening; gene expression; breast cancer; prostate cancer; nutriceutical; cosmetic; medical disorder; mental; biological; physiological; chemotherapeutic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine/threonine protein kinases, ribosomal protein kinases and cAMP-dependent kinases cDNA related to the invention
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Query Match Best Local Similarity

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Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.

Example 1; Fig 2; 310pp; English

and the procein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and/or cancers, cardiovascular disease, neuclador as immune-related diseases and/or cancers. The nucleic acids and neurodegenerative diseases and/or cancers. The nucleic acids and cassays. The kinase polypeptides may be used as antigens in the production of assays. The kinase polypeptides may be used as antigens in the production of annibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-citeress related disorders, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, portiasis, rhinitis, autoimmunity, diabetes, cancers and reproductive present sequence encodes a novel protein kinase. The nucleic acids disorders

Sequence 3224 BP; 820 A; 812 C; 769 G; 823 T; 0 U; 0 Other;

542 244 242 362 422 482 544 GGCTATTCCTTTGCTGTTGACTGGTGGTCGTGACGGCATATGAACTGCTGAGA 656 65 ArdddcddaAccacricccacaAgccccciciriridacdaAardaGaaGrahcrir 124 GACCACTTTGAAATTTTGCGAGCCATTGGGAAAGGCAGTTTTGGGGAGGTCTGCATTGTA 122 GACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCATCGTG 184 CAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAAAGTGCGTG 182 304 CCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCATGGTGGTG 302 364 425 GGGACTGTGAAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTAC 484 CACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTCCATG 604 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTC----AGCTCCAGAAAAGGAGCA 596 365 GACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTCACAGAG 424 62 CACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTT CAGAAGCGAGACATAAGAAATGTATGCAATGAAGTACATGAACAAGCAGAGAAGTGCATC GAGCGCAATGAAGTGAAATGTCTTCAAGGAACTCCAGATCATGCAGGTCTGGAGCAC GACCTCCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGGAACGTCCACTTCAAGGAA CACATCACAGATTTCAACATTGCTGCGATGCTGCCCAGGGAGACACAGATTACCATG 305 CCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTCATGGTGGTG GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACCAG CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACGTG GCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGGCCCC 3 ATGGGAGCGAACACTTCAAGAAACCACCAGTGTTTGATGAAAATGAAGATGTCAACTTT GAGAGGGATGAGGTTCGGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGAGCAC Gaps 6 Score 540.8; DB 4; Length 3224; Pred. No. 4e-139; 0; Mismatches 337; Indels 9; Query Match
Best Local Similarity 69.1%;
Matches 772; Conservative ( 485 545 543 125 123 185 423 483 605 63 183 245 243 303 363 597 g δ g 윰 ઠે 셤 ò 셤 ઠે 셤 ઠે 윱 ò g ઠે 셤 ò 유 ò ò

Claim 1; Page; 125pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human insulin resistance marker IRM210 (Ser/Thr protein kinase) cDNA #2.
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The invention relates to a method for diagnosing insulin resistance (IR), an IR-related condition, or susceptibility to IR or an IR-related condition, or susceptibility to IR or an IR-related condition in a patient. The method comprises detecting a difference in expression of at least one insulin resistance marker (IRM) in a biological sample from the patient, compared to the level of expression of the IRM in reference individuals who are not insulin resistant. The invention also encompasses screening for an agent to determine its usefulness in treating IR; the identification of a polymorphism section with an IR phenotype or risk of developining IR; estimating the frequency of a haplotype for a set of nucleotide polymorphism markers in a population; detecting an association between a haplotype and a phenotype; and identifying genes associated with a disease state. The methods of the invention are useful for diagnosing insulin resistance (IR), an IR-related condition, or susceptibility to IR or an IR-related conditions include hypertension, dysalpidaemia, types 2 diabetes, obesity or coronary artery disease. The methods are also useful in screening for agents useful in the treatment of these disorders. The in screening for agents useful in the treatment of these disorders. The shown in the specification, but was obtained from GenBank using the shown in the specification, but was obtained from GenBank using the accession number listed in Table 1 (page 25-33). 

Sequence 3224 BP; 820 A; 812 C; 769 G; 823 T; 0 U; 0 Other;

GAGCGCAATGAAGGAAATGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGCAC 242 482 542 596 GACCACTTTGAAATTTTGCGAGCCATTGGGAAAGGCAGTTTTGGGGAGGTCTGCATTGTA 122 CAGAAGAATGATACCAAGAAGATGTGCGCAATGAAGTACATGAATAAACAAAAGTGCGTG 182 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACCAG 422 664 GAGAGGGATGAGGTTCGGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGAGCAC 304 CCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCATGGTGGTG 302 CCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACGATGTTCATGGTGGTG GACCTCCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCACTTCAAGGAA 362 GGGACTGTGAAACTCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTAC 484 CACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTCCATG 604 CGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACGTG CACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTT CACATCACAGATTTCAACATTGCTGCGATGCTGCCCAGGGAGACACAGATTACCACCATG GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTC-----AGCTCCAGAAAAGGAGCA GCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGGCCCC GGCTATTCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACTGCTGAGA 3 ATGGGAGCGAACACTTCAAGAAAACCACCAGTGTTTGATGAAAATGAAGATGTCAACTTT 9; Gaps Score 540.8; DB 7; Length 3224; Pred. No. 4e-139; 36.4%; Score 5wv.v. 69.1%; Pred. No. 4e-139; Indels vive 0; Mismatches 337; Indels Best Local Similarity of Matches 772; Conservative Local Similarity 65 63 123 245 305 363 485 545 605 597 183 243 303 425 423 483 543 Query Match ઠે 8 g ò g 셤 g ઠે 셤 ક 유 ઠે g ઠે 셤 ઠે 쉱 ò Š ઠે

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Search completed: June 26, 2004, 21:12:27 Job time : 473 secs

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GenCore version 5.1.6
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June 26, 2004, 20:03:31 ; Search time 4048 Seconds (without alignments) 15900.298 Million cell updates/sec 6940544 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 gb ba: 4
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gb vi: 8 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Title: Perfect score: Scoring table: Database : Sequence: Searched: Run on:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 (bases 1 to 1485)
Ye,J., Yan,C., Di Francesco,V. and Beasley,E.M.
Isolated human kinase proteins
Patent: US 6653117-A 1 25-NOV-2003;
Location/Qualifiers
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Sequence 1 from patent US 6653117.
AR432044.1 GI:40194241

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Pred. No. 2.1e-296;
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                                        407 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCAGAACC
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                                                                                                                                          827 TACTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGT
                                                                                                  AGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACG
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               287 ACCCTTTCCTGGTTAATTTGTGGTATTCCTTCCAAGATGAGGAAGACATGTTCATGGTGG
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                   Plowman, G., Whyte, D., Manning, G., Sudarsanam, S. and Martinez, R. Human protein kinases and protein kinase-like enzymes Patent: WO 0155356-A 1 02-AUG-2001; Sugen, Inc. (US)
                                                                                                                                                                                                                                                                                                                                           61 TTGACCACTTTGAAATTTTGCGAGCCATTGGGAAAGGCAGTTTTGGGGAGGTCTGCATTG
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80.0%; Score 1188.2; DB 6.
Best Local Similarity 99.7%; Pred. No. 2.7e-286;
Matches 1190; Conservative 0; Mismatches 3;
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1. 1594
Organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
Sequence 1 from Patent WO0155356.
AX207388
AX207388.1 GI:15395198
                                                    Homo sapiens (human)
Homo sapiens
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GAGCGCAATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATGCAGGGTCTGGAGCAC 242
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    1191
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Sequence 10 from Patent WO0181557.
AX303185
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Hu,Y., Nepomnichy,B., Wang,X. and Donoho,G.
Human kinase proteins and polynucleotides encoding the same
Patent: US 6617147-A 10 09-SEP-2003;
Location/Qualifiers
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99.7%; Pred. No. 8.4e-286;
iive 0; Mismatches 3;
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                           Sequence 10 from patent US 6617147.
                                                                                                                                                                                                                    /organism="unknown"
/mol_type="genomic DNA"
                                                      AR393903
AR393903.1 GI:40121079
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.7
Matches 1188; Conservative
                                                                                                           Unknown.
Unclassified.
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                                        DEFINITION
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Walke,D.W.
Human kinase proteins and polynucleotides encoding the same Patent: WO 0181557-A 10 01-NOV-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.9%; Score 1186.2; DB 6; Length 1191; 99.7%; Pred. No. 8.4e-286; ive 0; Mismatches 3; Indels 0;
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                          Homo sapiens (human)
Mamo sapiens
Bukaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominides; Homo.
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99.7%; Pred. No. 2.1e-285;
tive 0; Mismatches 4;
                                                                                          Meyers, R. and Hunter, J.J.

14911 novel protein kinase molecules and
Patent: WO 0181589-A 3 01-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
 GI:17902482
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Best Local Similarity 99.7
Matches 1187; Conservative
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PAT 14-DEC-2001

linear

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AX320936 1191 bp Sequence 3 from Patent WO0181589. AX320936

RESULT 8
AX320936
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
TGGACCTCCTGCTGGGTGGAGCCTGCGTTATCACCTGCAACAAGAAGGTCCACTTCAAGG
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28quence 12 from Patent W00181557.

AX303187

AX303187.1 GI:17383669
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                                          ATGAATGATATAAACTGGGATGCAGTTTTTCAGAAGAGGCTCATTCCAGGTTTCATTCCT
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Hu,Y., Nepomnichy,B., Wang,X. and Donoho,G.
Human kinase proteins and polynucleotides encoding the same
Patent: US 6617147-A 12 09-SBP-2003;
Location/Qualifiers
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Best Local Similarity 98.8%; Pred. No. 6.9e-280;
Matches 1171; Conservative 0; Mismatches 14;
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/organism="unknown"
/mol_type="genomic DNA"
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711 TGGACCTCCTGCTGGGTGGAGACCTGCGTTATCACCTGCAACAGAACGTCCACTTCAAGG
                                           361 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGATGAGGCCCTGGAACTACCTGCAGAACC
                                                                     AAGAAACAGTGAAAGCTCTTCATCTGTGAGCTGGTCATGGCCCTGGACTACTGCTGCAGGAACC
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Human kinase proteins and polynucleotides encoding the same
Patent: US 6617147-A 8 09-SEP-2003;
Location/Qualifiers
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Sequence 8 from patent US 6617147.
AR393902.1 GI:40121077
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              Hu,Y., Nepomnichy,B., Wang,X., Donoho,G., Scoville,J. and
Walke,D.W.
Human kinase proteins and polymucleotides encoding the same
Patent WO 101557-A 12 01-NOV-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
                                                                                                                                                                                                     Query Match 78.3%; Score 1162.6; DB 6; Length 1675; Best Local Similarity 98.8%; Pred. No. 6.9e-280; Matches 1171; Conservative 0; Mismatches 14; Indels 0;

    1675
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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                                                                                          Query Match 78.2%; Score 1160.6; DB 6; Length Best Local Similarity 98.8%; Pred. No. 2.2e-279; Matches 1169; Conservative 0; Mismatches 14; Indels
                      1. .1224
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Lexicon Genetics Incorporated (US)
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Pukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoro, J., Isono, Y., Kawai-Hio, Y., Satio, K., Nishikawa, T., Kimura, K., Yamashita, H., Wagatsuma, M., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Rahehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., NBOO human cDNA sequencing project
                     AGCGCATCATTCACAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACG
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                          332 CCATGGGAGCCAACACTTCAAGAAAACCACCAGTGTTTGATGAAAATGAAGATGTCAACT
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Matches 1033; Conservative
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AK094580 2063 bp mRNA linear PRI 15-JUL-2002
Homo sapiens cDNA FLJ37261 fis, clone BRAMY2010464, moderately
similar to Mus musculus mRNA for serine/threonine protein kinase.
AK094580.1 GI:21753667
oligo capping; fis (full insert sequence).
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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AX166513
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2E (bases 1 to 2063)

S laggai,T and Yamamoto,J.

Direct Submission

AL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(B-mail:genomics@hri.co.jp, Teal:81-438-52-3975, Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5' = 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center etc.); 5' = 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center (PAB):

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

1. 2063

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Best Local Similarity 99.4
Matches 1033; Conservative
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Worl human protein kinases and protein kinase-like enzymes
Patent: WO 0138503-A 4 31-MAY-2001;
Sugen, Inc. (US)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                              1052 CGACTGTTGTAACTTACCCTTCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGC
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                                                 992 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGA
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661 GGAGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTTGAGA
                                                                                                            721 CGACTGTTGTAACTTACCCTTCTGCCTGGTCACAGGAAATGGTGTCACTTCTTAAAAAGC
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Search completed: June 26, 2004, 22:20:15 Job time : 4053 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 25, 2004, 10:47:04; Search time 44 Seconds
(without alignments)
2839.664 Million cell updates/sec
104
Sequence: 104
Sequence: 1 MGANTSRKPPVFDENEDVNF......NLALEQTKDPQGEDCQNNML 396
Scoring table: BLOSUM62
Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Cuery No. Score Match Length DB ID Description

2 1726 82.0 368 11 QPTPQ4 Q7tpQ4 mus musculu Q7tpQ5.5 67.8 414 11 Q9tpQ7 Q8tq0 mus musculu Q8ty14 homo sapien Q117.5 67.6 418 1 Q9tQ5 Q8tq0 mus musculu Q8ty14 homo sapien Q8ty16 mus musculu Q8ty16 mus musculu Q8ty17 homo sapien Q8ty17 62.9 486 1 Q9tQ5 Q8tq0 mus musculu Q8ty18 d8ty18 d9ty18 d9ty18 mus musculu Q8ty18 d1 Q8ty18 d1 Q8ty18 mus musculu Q8ty18 musculu M8 musculu

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Q96WJ8 Q814W3 Q43380 Q8MYP1 Q9TXB8	QBLPC1 Q25115 Q9Y777 097116 097115	097114 042793 QBNIK8 Q16957	09HGS0 09P466 08J129 07Z3Z7 07Y0L2	Q7YQL1 Q9BR29 Q16933 Q90WN3 Q96UM3	096338 Q8WW06 Q9MZD8 Q01143
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)

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TISSUE-Olfactory epithelium;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=124.7932;

MEDLINE R.D., Colling F.S., Medner L., Schaefer C.F., Bhat N.K., Anternan N., Max S.I., Wang J., Hsich F., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Anternan R.J., Malek J.A., Gunaratne P.H., Anternan R.J., Malek J.A., Gunaratne P.H., Antilalon D.K., Muzny D.M., Sodergren B.J., Iu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rrzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Anternan M., Marra M.A., Tonchman J.W., Green E.D., Dickson M.C., Schein J.E., Schnerch A., Schein J.E., Anternan M., Marra M.A.; Tonchman J.W., Smallus D.E., Schnerch A., Schein J.E., Anternan M., Marra M.A.; Tonchman J.W., Smallus D.E., Schnerch A., Schein J.E., Anternan M., Marra M.A.; Tonchman J.W., Green E.D., Dickson M.C., Schein M. J., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Anternan M., Anternan M., Marra M.A.; Tonchman J.W., Smallus M. I., Schein J. J., Marra M.A.; Tonchman J.W., Smallus M. I., Schein J.E., Schnerch A., Schein J.E., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., 
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                                                                                                                                                                                                                                                                                    MGANTSSKAPVFDENEDVNFDHFEILRAIGKGSFGKVCIVRKNDTKKMYAMKYMNKQKCV
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                                                                                                                                                                                                                                                       1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
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                                                                                                                                       Query Match 90.3%; Score 1899; DB 11; Length 398; Best Local Similarity 89.7%; Pred. No. 2.5e-150; Matches 357; Conservative 22; Mismatches 17; Indels 2.
PS00107; PROTEIN KINASE_ATP; 1.
PS50011; PROTEIN KINASE_DOM; 1.
PS00108; PROTEIN KINASE_ST; 1.
398 AA; 46509 MW; 689BCASB25CF18BB CRC64;
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OTTPQ4;
OTTPQ4;
O1-OCT-2003 (TrEMBLrel. 25, Created)
O1-OCT-2003 (TrEMBLrel. 25, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last amoration update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 IFNREKVNRDFNKRQPNLALEQTKD--PQGEDGQNNNL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 IFNREKVKSDFNQRQANLALEQTKONYTEEEEDGQNNNL 398
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                          PROSITE;
PROSITE;
                                                                                  SEQUENCE
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Q7TPQ4
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SIGURNE-22388257; PubMed=12477932;

A BIALINE-22388257; PubMed=12477932;

A RIABBERT R.D., Feligold B.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B tapleton M.J., Josdin T.B., Toshiyuki S., Carninci P., Frange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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                                                                                                                                                                                                                                                                             61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFWVVDLLLGGDLRYHLQQNVHFKE
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                      32;
                                                                                                                                                                                 Length 368;
                                                                                                                                                                                                                        Indels
                                                                    Strausberg R.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2003) to the EMBL; BCOSSO02; AAHSSO02.1; Hypothetical protein Protein Brown 368 AA; 43213 MW; ODB7F6977C39BB56 CRC64; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 IFNREKVKSDFNQRQANLALEQTKNNTEEBEDGQNNNL 368
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Last annotation update)
                                                                                                                                                                                 Query Match 82.0%; Score 1726; DB 11;
Best Local Similarity 82.9%; Pred. No. 6.6e-136;
Matches 330; Conservative 19; Mismatches 17;
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                                   SEQUENCE FROM N.A.
TISSUE=Olfactory epithelium;
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Q7TMD3;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 69.7% Matches 278, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Q8C4E0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 IPNKGRLNCDPTFELEEMILESKPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDSVQK 357
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MEDLINE=20164318; PubMed=10700184;
MEDLINE=20164318; PubMed=10700184;
Ruiz-Perez V.L., Ide S.B., Strom T.M., Lorenz B., Wilson D., Woods K.,
King L., Francomano C., Freisinger P., Spranger S., Marino B.,
Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skaleka U., Smailus D.B., Schnerch A., Schein J.B., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ERDEVRNVPRELQIMQGLEHPFLVNLWYSFQDEEDMFWVVDLLLGGDLRYHLQQNVHFTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGGNHSHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKYYAMKYYMKQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGANTSRKPPVFDENEDVNFDHPEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 ETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGF
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.4%; Score 1438.5; DB 11; Length 414; 68.5%; Pred. No. 8.1e-112; tive 39; Mismatches 71; Indels 19;
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022404; AAH52404.1; -.
EMBL; BC056396; AAH56396.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 414 AA; 47916 MW; 3C394415790594F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 68.5%
Matches 280; Conservative
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                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=C57BL/6;
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61 ERDEVRIVYFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQIVHFTE 120
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                                                                                                                                                                                                              MGD; MGI.1927522; Stk32.

R GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006464; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00229; Ser_thr_pkinase.
InterPro; IPR00229; Ser_thr_pkinase.
R Probom; PD000001; Prot kinase; 1.
R PROSITE; PS00107; PROTEIN KINASE ATP; 1.
R PROSITE; PS00107; PROTEIN KINASE DOW; 1.
R PROSITE; PS00108; PROTEIN KINASE DOW; 1.
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
W ATP-binding; Kinase; Serine-fitheonine-protein kinase; Transferase.
G SEQUENCE 414 AA; 47917 MW; BE394415790B9A13 CRC64;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
"Mutations in a new gene in Ellis-van creveld syndrome and Weyers acrodental dysostosis.";
Nat. Genet. 24:283-286(2000).
-- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AJZ50840; CAB76566.1; --
HSSP; P05132; LCTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.3%; Score 1437.5; DB 11; Length 414; 69.7%; Pred. No. 9.8e-112; ive 38; Mismatches 64; Indels 19;
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Last annotation update)
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
A the RIKEM Genome Exploration Research Group Phase I & II Team;
Than Tygis of the mouse transcriptome based on functional annotation of RT 60,770 full-length cDNAs.";
INELE ACCOSS-373(2002).
BR MGD; MGI:1927552; Stk32.
BR MGD; MGGG468; Pripotein amino acid phosphorylation; IEA.
BR MGGG468; Pripotein amino acid phosphorylation; Pripotein
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 68.2%; Pred. No. 1.7e-111;
Matches 279; Conservative 40; Mismatches 71;
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TISSUE=Brain;
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R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005404; F:Drotein serine/threonine kinase activity; IEA.

R GO; GO:000646; P:Drotein amino acid phosphorylation; IEA.

R GO; GO:000646; P:Drotein amino acid phosphorylation; IEA.

InterPro; IPR00219; Prot kinase.

R InterPro; IPR008271; Ser thr pkinase.

R ProDon; PR000601; Prot kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE DOW; 1.

R PROSITE; PS01017; PROTEIN KINASE DOW; 1.

R PROSITE; PS01017; PROTEIN KINASE STP; 1.
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                                           D., Woods ?
no B.,
MEDLINE=20164328; PubMed=10700184;

Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods

King L., Francomano C., Freisinger P., Spranger S., Marino B.,

Dallapiccola B., Wright M., Meltinger T., Polymeropoulos M.H.,

Goodahip J.;

"Mutations in a new gene in Blis-van Creveld syndrome and Weyers
acrodental dysoscosis.";

Nat. Genet. 24:283-286 (2000).

- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

BMBL; AJ250839; CABF6471.1;

HSSP; PO5132; ICTP.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Gene for serine/threonine protein kinase.
Memo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Q9JJG4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 VPNKGRLNCDPTPELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPLNGHLQHCLETVRE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGGNHSHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMNKQKCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AGTKPYMAPEVFQVYMDGGPGYSYPVDWWSLGITAYELLRGWRPYELHSVTPIDBILLNWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 BRNEVRNVPKELQIMQGLEHPPLVNIMYSPQDEEDMPMVVDLLLGGDLRYHLQQNVHPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 BTVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AGTKPYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 ETTVVTYPSAWSQEMVSLLKKALLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGANTSRKPPVFDENEDVNFDHFBILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
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                                        Straubberger,
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005524; R:ATP binding; IRA.

GO; GO:0004674; F:Protein serine/threonine kinase activity; IRA.

GO; GO:0004613; F:protein-Tyrosine kinase activity; IRA.

GO; GO:0004648; P:protein amino acid phosphorylation; IRA.

InterPro; IPR00129; Prot kinase.

InterPro; IPR00129; Ser_thr_Dkinase.

InterPro; IPR00129; Ser_thr_Dkinase.

InterPro; IPR00129; Tyr_pkinase.

R Probom; PR00129; Prot kinase; 1.

R RAMRT; SM00220; S TKC; 1.

R RAMRT; SM00219; TyrKc; 1.

R ROSITE; PS00101; PROTEIN KINASE DAP; 1.

R PROSITE; PS00101; PROTEIN KINASE DAW; 1.

R ROSITE; PS00107; PROTEIN KINASE DAW; 1.

R ROSITE; PS00108; PROTEIN KINASE STP 1.

R RAMART; SM00220; S TKC; 1.

R ROSITE; PS00108; PROTEIN KINASE DAW; 1.

R ROSITE; PS00108; PROTEIN KINASE DESEGSSERAS42F CRC64;
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Ma A.-H., Nelson D.A., Xia L., Ravi L., Chen H.-C., Robinson D.R.,
Kung H.-J.;
"PKE, A New Human AGC Group Kinase, Phosphorylates SET, a PP2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.6%; Score 1421.5; DB 4; Length 414; Best Local Similarity 68.2%; Pred. No. 2.1e-110; Matches 275; Conservative 43; Mismatches 78; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFIIFNREKVNRDFNKRQPNLALEQTKDPQG----EDGQNNNL 396
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SEQUENCE PROM N.A.
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72 MSAATARR-PVFDDKEDVNFDHFQILRAIGKGSFGKVCIVQKRDTEKNYAMKYMKKQQCI 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 STVSVOYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPGF
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             EMBL, AVO98866; AAM21719.1; -
SUDDIATEGE (AFK-2002) TO THE EMBL/Genbank/DDBJ Gatabases.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:Protein serine/chreonine kinase activity; IEA.

GO; GO:0004671; F:protein serine/chreonine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR00129; Prot kinase.

InterPro; IPR00129; Ser_chr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Frodon; PD000001; Prot Kinase; 1.

SWART; SM00220; STKc; 1.

R SWART; SM00220; STKc; 1.

R PROSITE; PS00107; PROTEIN KINASE_DOM; 1.

R PROSITE; PS00104; PROTEIN KINASE_ST; 1.
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09JJG4,
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Brain cDNA, clone MNCb-1563, similar to AJZ50840 serine/threonine
Protein kinase (Mus musculus).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.9%; Score 1324; DB 4; Length 486;
Best Local Similarity 64.5%; Pred. No. 3.7e-102;
Matches 254; Conservative 53; Mismatches 77; Indels 10;
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STRAIN=CSTBL;
Sadda N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano
Habhimoto K.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 AA; 54994 MW; 38FEFBB3863B21F3 CRC64;
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Q96BA3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 TYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIPNKG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 QYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPSLAHVLMDDLSEKKVEPGFVPNKG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNVFKELQIMQGLEHPPLVNLWYSPQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 FICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YMAPEMFSS--RKGAGYSPAVDWWSLGVTAYBLLRGRRPYHIRSSTSSKEIVHTFETTVV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RINCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSSQT--CLLQEHLDSVQKEFII 361
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MGD; MG1:238536; Pke.

R GO; GO:0005524; P:ATP binding; IEA.

GO; GO:0004674; P:Drotein serine/threonine kinase activity; IEA.

GO; GO:0004674; P:Protein serine/threonine kinase activity; IEA.

GO; GO:0004648; P:Protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:Protein amino acid phosphorylation; IEA.

InterPro; IPR00219; Por thinase.

R InterPro; IPR00219; Per thr pkinase.

R Probom; P000060; Pkrot kinase.

R PRODOM; P00010; Prot kinase; 1.

R PROSITE; PS00101; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 SRKPPVFDENEDVNPDHFBILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVBRNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
  "Isolation of full-length cDNA clones from mouse brain cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
               62.6%; Score 1317.5; DB 11; Length 488;
64.3%; Pred. No. 1.3e-101;
tive 54; Mismatches 76; Indels 9;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical gerine/threonine protein kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNREKL----KRSQELMSEPPPGPETSD 460
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080ZV4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
STRAIN=C57BL/6J; TISSUB-Brain; MEDINE=22354683; PubMed=12466851; The PANTOM CONSOrtium, The PANTOM CONSOrtium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; 60,770 (tull-length CDNAs."; Panalysis of the mouse transcriptome based on functional annotation of 60,770 (tull-length CDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 FICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMJPRETQITTMAGTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YMAPEMFSS--RKGAGYSFAVDWWSLGVTAYBLLRGRRPYHIRSSTSSKEIVHTFETTVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 RIVVPXELOIMQGLEHPPLVNI, WYSPQDEEDMPMVVDLLIGGDLRYHLQQNVHPKBETVKL
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                                                                                                                                                                                                                                                                        R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0006674; F:Drotein serine/threonine kinase activity; IEA.

R GO; GO:000664; F:Protein serine/threonine kinase activity; IEA.

R GO; GO:0006466; P:Protein amino acid phosphorylation; IEA.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR00220; Ser thr pkinase.

R Pfam; PF00069; pkinase; I.

R Prodom; PD000001; Prot kinase; I.

R PROSITE; PS00107; PROTEIN KINASE ATP; I.

R PROSITE; PS00107; PROTEIN KINASE DOM; I.

R PROSITE; PS00101; PROTEIN KINASE DOM; I.

R PROSITE; PS01001; PROTEIN KINASE ST; I.

R HYPOTHERICAL PROTEIN KINASE ST; I.

R HYPOTHERICAL ATP-DINGING; Kinase;

SEQUENCE 488 AA; 55262 MW; 2B6A927BE6B78EF2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.6%; Score 1317.5; DB 11; Lengt
Best Local Similarity 64.3%; Pred. No. 1.3e-101;
Matches 250; Conservative 54; Migmatches 76; Indele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 FNREKVNRDFNKRQPNLALEQTKDPQGED 390
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                                                                                                                                                                                                                          EMBL; BC026457; AAH26457.1; -. EMBL; AK046439; BAC32730.1; -.
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Q96BA3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LRYHLQQNVQFSEDTVRLYICEMALALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 AAMLPRETQITTMAGTKPYMAPEMPSS--RKGAGYSFAVDWWSLGVTAYELLRGRRPYHI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 RSSTSSKEIVHTPETTVVTYPSAMSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDIN 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLEKLLTVNDEHRLSSLQDVQAAPALAGVL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDAVPQKRLIPGFIPNKGRLNCDPTFELEEMILESKPLHKKKKRRLAKKEKDMRKCDSSQT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 WDHLSEKRVEPGFVPNKGRLACDFTFELEEMILESRPLHKKKGRLAKNKSRDNSRDSSQS 300
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                                                                                                        Tilsoughergr R.;
Strausbergr R.;
Strausbergr R.;
Strausbergr R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Thirthy BELOMOS TO THE SER/THR FAMILY OF PROTEIN KINASES.
RMEL; BC015792; AAH15792.1; --
DR GO; GO:00005524; F:ATP binding; IEA.
DR GO; GO:0000674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016740; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR Flem; PF00069; pkinase; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS50011; PROTEIN KINASE ST; 1.
KW Hypothetical protein; ATP-Dinding; Kinase;
Serine/threonine-protein.
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MEDLINE-2238825; PubMed=12477932;
MEDLINE-2238825; PubMed=12477932;
Strauberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
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6
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 54.1%; Score 1137.5; DB Best Local Similarity 62.8%; Pred. No. 9.9e-87, Matches 218; Conservative 47; Mismatches 73
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                                                              SEQUENCE FROM N.A.
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MCBI_TaxID=9606;
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rokrigues S., Banchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalakka U., Smailus D.E., Schnerch A., Schein J.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MYAMKYMNKQQCIERDEVBVVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 --CLLQEHLDSVQKBFIIFNREKVNRDFNKRQPNLALEQTKDPQGED 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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             McMurray A.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 WGHLSEKRVEPDFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 MCAMKYMNKQKCVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 AAMLPRETQITTMAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGVTAYELLRGRRPYHI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 RSSTSSKEIVHTFETTVVTYPSAMSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDIN 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                 TISSUE=Frontal cortex;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MYAMKYMOKQQCIERDEVRNVFRELGILQEIEHVPLVNLWYSFQDEEDMFMVVDLLLGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LRYHLQQNVQPSEDTVRLYICEMALALDYLCGQHIIHRDVKPDNILLDERGHAHLTDFNI
                                                                                                                                                                                                                                                                            Interview. ";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

- :- SIMILARITY: BELCOUSS TO THE SER/THR FAMILY OF PROTEIN KINASES.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000574; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006746; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006746; F:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPRO02719; Prot kinase.

R InterPro; IPRO02719; Ser Lhr Dkin AS.

R Am: PRO0109; Prot kinase; 1.

R PROSITE; PSO0101; Prot Kinase; 1.

R PROSITE; PSO0101; PROTEIN KINASE DW; 1.

R PROSITE; PSO0108; PROTEIN KINASE ST; 1.

R PROSITE; PSO0108; PROTEIN KINASE ST; 1.

R PROSITE; PSO0108; PROTEIN KINASE ST; 1.

R PROFICE AS ST CAS ST CAS ST CAS ST CAS SECULE CRC64;

SEGUENCE 366 AA; 42218 MW; 5D7269B32DABCC14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 ENDYLQDCLDAIQQDFVIFNREKL----KRSQDLPSEPLPAPEPRD 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 --CLLQEHLDSVQKEFIIFNREKVNRDFNKRQPNLALEQTKDPQGED 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.4%; Score 1122.5; DB 6; Length
62.8%; Pred. No. 1.8e-85;
ive 44; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 62.8
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                            NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q21483
Q21483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
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142 IIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTWAGTKPYWAPEWFSS--RKGAG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 YSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVVTYPSAWSOEMVSLLKK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 LLEPNPDORFSQLSDVONFPYMNDINWDAVFOXGLIPGFIPNKGRLNCDPTFELEEMILE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLVNLWYSPODEEDMFMVVDLLLGGDLRYHLOONVHFKEETVKLFICELVMALDYLONOR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 HPSVIRSIGRGAPGKVCIVQERKTKKYPALKYMNKRRCIEKGVAANVIRELTLLSKMSHP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 SKPLHKKKKKRLAKKEKDMRKCDSSQTCLLQEHLDSVQKRFIIFNREKVNRDFNKRQPN 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STPIH--RRKTWHNNSSGRSSSEPQNAALVE----VSKAFIDFSRHNV-----KIEPN 373
                                                                                                                                                                                                                                                                                                                                                                                                              R Wormbep; M03C11.1; CE03492.

R GO; GO:0006524; F:ATP binding; IEA.
GO; GO:0006474; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
R InterPro; IPR000719; Prot kinase.
R InterPro; IPR00220; Ser_thr_pkinase.
R InterPro; IPR008271; Ser_thr_pkinase.
R Probom; PD000001; Prot kinase; 1.
R PROBOM; PROCO001; Prot kinase; 1.
R PROSITE; PS00107; PROTEIN KINASE DOW; 1.
R PROSITE; PS00107; PROTEIN KINASE DOW; 1.
R PROSITE; PS00109; PROTEIN KINASE ST; 1.
R PROSITE; PS00109; PROTEIN KINASE ST; 1.
C PROSITE; PS00109; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 HFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNBVRNVFKELQIMQGLEHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; 249128; CAA88953.1; -.
PIR; T23688; T23688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 379;
                                                                                                                                                                         Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indele
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to serine threonine kinase 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.1%; Score 843.5; DB 5; Best Local Similarity 44.1%; Pred. No. 3.8e-62; Matches 158; Conservative 70; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 AA
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                                                                      SEQUENCE FROM N.A.
MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] =
SEQUENCE FROM N.A.
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61 ERNEVRNVPKELQIMQGLEHPFLVNLWYSFQDEEDMFWVVDLLLGGBLRYHLQQNVHFKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 BRNBVRNVFKELQIMQGLEHPFLVNLMYSFQDBEDMFMVVDLLLGGDLRYHLQQNVHFKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGANTSRKPPVPDENEDVNFDHFEILRAIGKGSFGKVCIVQKNDTKKMYAMKYMNKQKCV 60
                A STRANDED MAINTY CLAUSE;

STRANDED MAINTY CLAUSE;

SUBMITTED (JAN-2002) to the EMBL/GenBank/DDBJ databases.

-1- SIMDIARITY: BELONGS TO THE SER/THR PAMILY OF PROTEIN KINASES.

EMBL; BCO166; AAH12666.1; -.

R GO; GO:0004674; F:PROTEIN SITEM-(Threonine Kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

R D:DOON; PROUGHJ; PROTEIN KINASE ATP; 1.

R ROSITE; PSO0101; PROTEIN KINASE DOW; 1.

R ROSITE; PSO0101; PROTEIN KINASE DOW; 1.

R ROSITE; PSO0101; RROTEIN KINASE DOW; 1.

R ROSITE; PSO0101; RROTEIN KINASE DOW; 1.

R ATP-binding; Kinase; Serime(threonine-protein kinase; Transferase.)

SEQUENCE 166 AA; 19792 WW; CDCF94E54C793BA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGFVCIVQKNDTKKMCAMKYMNKQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.1%; Score 822; DB 4; Length 166; Best Local Similarity 98.7%; Pred. No. 8e-61; Matches 155; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: June 25, 2004, 10:51:07 Job time : 46 secs
TISSUE=Urinary bladder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 25, 2004, 10:43:09; Search time 18 Seconds (without alignments) 1145.543 Million cell updates/sec

US-10-667-442-2 2104 1 MGANTSRKPPVPDENEDVNF......NLALEQTKDPQGEDGQNNNL 396 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

141681 segs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		عد			SUMMARIES			
Result No.	Score	Query Match	Query Match Length	DB	ΙD	BCT	ption	
-	582.5	27.7	444	-	KRAC DICDI	P54644	dictyosteli	
~	537	25.5	479	ч	PK2 DICDI	P28178	dictyosteli	
m	528.5	25.1		7	KAPC DICDI	P34099	dictyosteli	
4	519	4.		-1	KP19 ARATH	039030	arabidopsis	
Ŋ	516.5	24.5		7	KPK1 ARATH	P42818	arabidopsis	
9	513	24.4	680	Н	YPK1_YEAST	P12688	saccharomyc	
7	511.5	24.3	969	٦	SCK1_SCHPO	P50530		
80	510.5	24.3	352	Н	KAPC_DROME	P12370	drosophila	
σ	503	23.9		٦	KAPC_CAEBL	P21137		
10	502.5	23.9		Н	KAPA CRIGR	P25321	_	
11	502.5	23.		Н	KAPA_PIG	P36887	sus scrofa	
12	502.5	23.		Н	SCH9_YEAST	P11792	saccharomyc	
13	501.5	23.8	740	Н	K6A3_HUMAN	P51812	homo sapien	
14	501.5	23.		-	K6A3 MOUSE	P18654	mus m	
15	501	23.		~	YPK2_YEAST	P18961	Bacc	
16	500.5	23.		Н	KAPG HUMAN	P22612	homo	
17	500.5	23.		Н	K6A2 HUMAN	015349	рошо	
18	498.5	23.		Н	KAPA_CANFA	Q8mj44	cani	
19	498.5	23.		Н	KAPA HUMAN	P17612	homo sapien	
20	498.5	23.		-1	KAPA_RAT	P27791		
21	498.5	23.		-	KAPA_SHEBP	O9mzd9	ovis aries	
22	498.5	23.		-	ARK1 HUMAN	P25098	homo sapien	
23	496.5	23.		Н	KAPA_BOVIN	P00517	bos taurus	
24	496.5	23.		Н	K6A2 MOUSE	Q9wut3	m ribosomal	
52	496	23.		٦	KAPB MOUSE	P05206	mus musculu	
56	495.5	23.		Н	KPCI_MOUSE	Q62074	mus musculu	
27	495.5	23.		Н	KPCI HUMAN	P41743		
28	494.5	23.		٦	K6AA CHICK	P18652	-	
59	493.5	23.		~	KAPC_YEAST	P05986	_	
30	493.5	23.		Н	KUBE_SCHPO	010364	schizosacch	
31	493.5	23.	68	Н		P21146		
32	493	23.4	689	-	ARK1 MESAU	æ	mesocricetu	
33	492.5	23	350	7	KAPA_MOUSE	P05132	mus musculu	

P26817 rattus norv											
ARK1_RAT	K6AA_XENLA	KAPB SCHPO	K6AB_XENLA	K6A6 HUMAN	KAPB_YEAST	KAPB HUMAN	KAPB_BOVIN	KAPI_BOVIN	AKT3 HUMAN	AKT3 MOUSE	KAPB_PIG
-	-	-	н	н	Н	н	-	-	Н	н	-
689	733	512	629	745	380	320	350	397	479	479	350
23.4	23.4	23.3	23.2	23.2	23.1	23.1	23.1	23.1	23.1	23.1	23.1
	ß	90	8.5	17.5	487	86.5	486	486	85.5	85.5	485
492.5	491.	4	48	4		4			4	4	

## ALIGNMENTS

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                                                                                                                                                                                                                                                 # HSSP; PO5131; 1CTP.

# HSSP; PO5131; 1CTP.

# HSSP; PO5131; 1CTP.

# InterPro; IPR0003794; pkbA.

# InterPro; IPR000319; Prot kinase.

# InterPro; IPR00019; Prot kinase.

# InterPro; IPR0019; Prot kinase.

# InterPro; IPR00219; Ser thr pkinase.

# Pfam; PF00169; pkinase; 1.

# Pfam; PF00169; pkinase; 1.

# Pfam; PF000019; Prot kinase; 1.

# Pfam; PF00169; pkinase; 1.

# PROSITE; PS00109; PROTEIN KINASE ATP; 1.

# PROSITE; PS00119; PROTEIN KINASE DOM; 1.

# Transferase; Serine/Ehreonine-protein kinase; ATP-binding.

# DOMAIN 120 374 ATP (BY SIMILARITY).

# PROTEIN KINASE A13 BY SIMILARITY.

# ATT SITE 243 243 BY SIMILARITY.

# REQUENCE 444 AA; 51062 MW; 12367ALA411C5680 CRC64;
                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAZ-2004 (Rel. 43, Last annotation update)
RAC-family serine/threonine kinase homolog (EC 2.7.1.-).
                                                                                                                                    Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCB TaxID=44689;
                                    444 AA
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U15210; AAA76692.1; -.
                                    STANDARD;
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
RESULT 1
KRAC_DICDI
ID KRAC_DICDI
                                                                                                                                                                                                                                      STRAIN=AX3;
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                          9
                                                                         160
                                                                                                               EVRNVPKBLOIMOGLEHPPLVNLWYSPODEBDMFMVVDLLLGGDLRYHLQQNVHFKBBTV 123
                                                                                                                                                                                                   GTKPYMAPEMPSSRKGAGYSPAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETT 241
                                                                                                                                                                                                                                                   242 VVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIPN 301
                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 NTSRKPPVFDENEDVNFDHFBILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERN
                                                                281 GTPEYLAPEVL---QGNGYGKQVDWWSFGSLLYEMLTGLPPFY---NQDVQEMYRKIMME
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathway.
SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6
                          15;
  Length 444;
27.7%; Score 582.5; DB 1; Length 4 38.2%; Pred. No. 8.6e-33; ive 70; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
PKGB OR PFKA.
                                                                                                                                                                                                                                                                                                                                                                                         479 AA
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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InterPro; IPR000961, Pkinase_C.
InterPro; IPR000719, Prot_kinase.
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                                                                                                                                                                                                                                                                                                    302 -KGRLN---CDPTF 311
                                                                                                                                                                                                                                                                                                                           395 VKGSADTSQIDPVF 408
Ouery Match
Best Local Similarity 38.23
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 EVIN---GHGHGCAVDWWSLGTLLYEMLTGLPPFYSQNVSTMYQKILNGELKIPTY---I 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 IFSKNKQSATKDDFELLINVIĞKĞSFĞKVMQVKKKĞEDKIFAMKYLRKDAIIARKQVNHTK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 KELQIMQGLEHPPLVNLWYSPQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEBTVKLFICE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VPDEN-EDVNPDHPBILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNBVRNVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 LVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 KMPSSRKGAGYSPAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVVTYPSAW
R InterPro; IPR008271; Ser_thr_pkin_AS.
R InterPro; IPR001290; Ser_thr_pkinase.
R Fran; PR001245; Tyr_pkinase.
R Fran; PR001245; Tyr_pkinase.
R Pfan; PR00131; pkinase.
R PRINTS; PR00109; TYRKINASE.
R PRODOM; PR00109; Prot_kinase; 1.
R PROBOM; PR00131; STKC; 1.
R PR021TE; PS00103; PROTEIN KINASE ATP; 1.
R PR051TE; PS00101; PROTEIN KINASE ST; 1.
R PR051TE; PS00101; PROTEIN KINASE DOM; 1.
R PR051TE; PS0011; PR07EIN KINASE DOM; 1.
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EB0015C08E397105 CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CAMP-dependent protein kinase catalytic subunit (EC 2.7.1.37).
PXAC OR PK2 OR PK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.5%; Score 537; DB 1; Length 47
36.2%; Pred. No. 1.2e-29;
ive 66; Mismatches 124; Indels
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Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 ISQIDPVFTQERPMDSLVETSAL 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52963 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36.2%;
Matches 117; Conservative
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276
309
479 AA;
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CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
NP BIND
BINDING
ACT SITE
MOD RES
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KAPC_DICDI

KAPC_DICDI

AC P34099

DT 01-FEB

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DD CAMP-d

GN PKAC O

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLNSEKSILSSIHHPPEIVNLYQAPQDEKKLYLLFEYVAGGEVFTHLRKSMKFSNSTAKFY 439
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                                                                                                                                                                                                                                                                                                                                                                                               a maximum at culmination.
SIMILARITY: Belongs to the Ser/Thr family of protein kinases, CAMP
                                                                                                                                                                     Mann S.K.O., Yonemotor W.M., Taylor S.S., Firtel R.A.;

Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.;

"DdPK3, which plays essential roles during Dictyostelium development,
encodes the catalytic subunit of CAMP-dependent protein kinase.";

Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).

-!- FUNCTION: Essential for differentiation and fruit morphogenesis.

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-!- CAMPITI IN DICTYOSTELIUM THE HOLORMIXTME IS A DIMER COMPOSED OF
A REGULATORY (R.) AND A CATALYTIC (C.) SUBUNIT. IN THE PRESENCE OF
CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT. AND AN R MONOWER.

-!- DEVELOPMENTAL STAGE: CAPK activity is low in vegetatively growing amobeae, increases during development of aggregation and reaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 PPV---NARBRLKBFKQIRVLGTGTFGKVYLIQ--NTKDGCYYAMKCLNKAYVVQLKQVB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.1%; Score 5.20.9; --. 34.2%; Pred. No. 6.60-29; tive 76; Mismatches 115; Indels 21; Gaps tive 76; Mismatches 115; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DictyBace; DDB0003193; pkaC.

R InterPro; IPR000961; Pkinase_C.

R InterPro; IPR000821; Proc kinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; Pr004033; pkinase; 1.

R Pfam; Pr004033; pkinase; 1.

R PRMTS; PR001001; Prot kinase; 1.

R SMART; SM00130; TrK; INTASE AIP; 1.

R PROSITE; PS00100; PROTEIN KINASE AIP; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R Transferase; Serine/threomine-protein kinase; ATP-binding; CAMP;
MEDLINE=93385090; PubMed=8373760; Anjard C., Etchebehere L., Pinaud S., Veron M., Reymond C.D.; Anjard C., Etchebehere L., Pinaud S., Veron M., Reymond C.D.; Mn unusual catalytic subunit for the cAMP-dependent protein kinase of Dictyostellum discoldeum."; Biochemistry 32:9532-9538(1993).
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D0F9B3A48C58D084 CRC64;
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THR-RICH.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                      STRAIN=AX3;
MEDLINE=93066311; PubMed=1332055;
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HSSP; P05132; 1ATP.
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MOD RES
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BINDING
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TOO Lumbia;

RA SALAN-E-V. Columbia;

RA SALAN-E-V. Columbia;

RA SALAN-E-V. Columbia;

RA SALAN-E-V. Columbia;

RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B., Balanoubat M., Cartolico L., Weissenbach J., Saurin W., Quetier F., Boester C., Brottier P., Robert C., Enchtier P., Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F., Schaefer M., Mangler Auer S., Gabel C., Fuchs M., Bangert B., Wincker P., Drzonek H., Erfle H., Jordan N., Bangert B., Warmbach B., Drzonek H., Farfer H., Jordan R., Brandt P., Nyakatura G., Wurmbach B., Drzonek H., Kauer G., Lochnert T.-H., Nordsiek G., Conrad A., Hornischer K., Kauer G., Lochnert T.-H., Nordsiek G., Conrad A., Hornischer K., Schoen O., Bargues M., Terol J., Climent J., Collado C., Perez-Perez A., Ottenwaedber B., Duchemin D., RA Navarro P., Collado C., Perez-Perez A., Ottenwaedber B., Duchemin D., RA Marro P., Collado C., Perez-Perez A., Ottenwaedber B., Many D., Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Many D., Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Many D., Cooke R., Laudie M., Schoef H., Kude S., Zaccaria P., Marren B., Razo M., Waltes M., Nierman W.C., Salzberg E., White O., Venter J., Crass T.H., Haas B. Maiti R., Wu D., Pererson J., Van Aken S., Crass D., Linh X., Nierman W.C., Salzberg S.L., Milte O., Venter J.C., Fraser C. M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu B., Kimura T., Idesawa K., Kawashima K., Kishida Y., Rigeren C. M., Kaneko T., Nakamura S., Nakazaki N., Saneko S., Yamada M., Tabata S., Nakatanabe A., Yamada M., Tabata S., Nakatanabe A., Yamada M., Tabata S., Recondance and analysis of chromesome J of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                     247 SAWSQEMVSILKKILEPNPDQRPSQLS----DVQNFPYMNDINWDAVFQKRLIPGFIPNK 302
                                                                                                                                                                                                                                                                                                                                              497
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MRA-2004 (Rel. 43, Last sequencion update)
Serine/threonine-protein kinase AtPK19 (EC 2.7.1.-) (Ribosomal-protein ATPK19 OR AT3G08720 OR F17014.19.
ATPK19 OR AT3G08720 OR F17014.19.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
127 ICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPY
                                                                                                                                                                                               :|||: |: |: |: |||||:||: |: |: | | |:: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |: | 3 |
                                                                                                                                                  187 MAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTPETTVVTYP
                                        "Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold or salinity stress in Arabidopsis thaliana."; FEBS Lett. 358:199-204(1995).
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STRAIN=cv. Columbia;
MEDLINEE-95129712; PubMed=7828736;
MizOguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
Shinozaki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 GRINCOPTFEL--EEMILESKP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KP19 ARATH
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE PROM N.A.

SEQUENCE Columbia;

X MEDLINE=29294869; PubMed=14593172;

X MEDLINE=29294869; PubMed=14593172;

A Rarlin-Newmann G. Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Hayashizaki Y., Johnson-Hopson C., Hauan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A Kamiya A., Meyers C., Nakajima M., Narusaka M., Sakurai T.,

Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: May be involved in adaptation of plant to cold or high-salt conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6
                                                                                                                                  STRAIN=cv. Columbia;
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J. Theologis A., Ecker J., Davis R.W.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinase subfamily.
-!- CAUTION: Ref.4 sequence differs from that shown due to a frameshift in position 391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95F007B44B58DFB5 CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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A -> V (IN REF. 1).
LS -> VF (IN REF. 1)
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InterPro; IPR000961; Pkinase C.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkin AS.
InterPro; IPR002290; Ser thr pkinase.
Pfam; PF00069; pkinase; I.
ProDom; PD000001; Prot Kinase; I.
SWART; SM0013; STK X; I.
SWART; SM0013; STK X; I.
PROSITE; P600107; PROTEIN KINASE ATP; I.
PROSITE; P600108; PROTEIN KINASE DOM; I.
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EMBL; AC012562; AAG51345.1; -.
EMBL; AF325094; AAK17162.1; -.
EMBL; AY050826; -; NOT_ANNOTATED_CDS.
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                               Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 302:842-846(2003)
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HSSP; P05132; 1CTP.
                                                                                                  SEQUENCE FROM N.A.
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BINDING
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24.7%; Score 519; DB 1; Length 471;

Query Match

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350 -KDKIKLPQPLSNEAHALLKGILQKEPERRLGSGPSGABEIKKHKWFKAINWKKCLBARBV 408
                                                                                                                                                                                                                                119 KEETVKC.FICELVMALDYLQNQRIIHRDWKPDNILLDEHGHVHITDFNIAAMLPRETQIT 178
                                                                                                                                                                                                                                                                                                                                                                                                  239 ETTVVTYPSAMSQEMVSILKKULEPNPDQRF----SQLSDVQNFPYMNDINWDAVFQKRL 294
                                                              12 PDENED------VNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salancubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
De Simone V., Choisne N., Artiguenave R., Robert C., Brottler P.,
Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Banes V.,
Winchelmann R., Kranz H., Srfle H., Jordan N., Bangert S.,
Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Myakatura G.,
Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
Conrad A., Hornlscher K., Kauer G., Loehnert T.-H., Nordslek G.,
                                                                                                                                                59 CVERNEVRNVFKELQIMQGLEHPFLVNLWYSPQDBEDMFMVVDLLLGGDLRYHLQQNVHF
                                                                                                                                                                                                                                                                                                                  179 TMAGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTF
                                                                                                                                                                                                                                                                                                                                        :||| ||||||: :||: |||||:|: ||:||:||: |:||: |::||
296 SMCGTTEYMAPEIV---RGKGHDKAADWWSVGILLYEMLTGKPPFLGSKGKIQQKIV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atauluopsis Lialiana (mouse-ear Cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang S.-H., Lawton M.A., Hunter T., Lamb C.J.;
"Atpkl, a novel ribosomal protein kinase gene from Arabidopsis. I.
Isolation, characterization, and expression.";
J. Biol. Chem. 269:17586-17592(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold or salinity stress in Arabidopsis thaliana."; FEBS Lett. 358:199-204(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-95129712; PubMed-7828736;
Mizoguchi I., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
Shinozaki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
5erine/threonine-protein kinase AtPKI/AtPK6 (BC 2.7.1.-).
ATPKI OR ATPK6 OR AT3G08730 OR F17014.20.
Arabidopsis thaliana (Mouse-ear cress).
34.0%; Pred. No. 2e-28;
:ive 64; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 AA.
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MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Landsberg erecta;
MEDLINE=94292519; PubMed=7912697;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 OPSFKPAVSGROCIANFD 426
                      Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
    Best Local Similarity
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P42818;
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Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., A navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D., Cooke R., Laudie M., Berger-Lilauro C., Purnelle B., Masuy D., A Ge Haan M., Maaree A.C., Alcasaz J.-P., Cottet A., Casacuberta E., Monfort A., Argirtou A., Flores M., Liguori R., Vitale D., Mamhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., R. Mayer K.P.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J., R. Rooney T., Rizzo M., Walts A., Utterback T., Fulit C.Y., Shea T.P., Creasy T.H., Haas B., Maitl R., Wu D., Peterson J., Van Aken S., A. Peid G., Miltscher J., Sallers P., Gill J.E., Feldblyum T.V., Raman W.C., Sallers S.L., White O., Venter J.C., Ramer D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Rasancto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muzaki A., Nakayama S., Nakazaki M., Shinpo S., Takeuchi C., Wada T., Matanabe A., Yamada M., Yasuda M., Tabata S.; Matanabe A., Yamada M., Yasuda M., Tabata S.; Lakeuchi C., Wature A., Shinpo S., Takeuchi C., Wada T., Matanabe A., Yamada M., Yasuda M., Tabata S.; Lakeuchi C., Wada T., Matanabe A., Watanabe A., Yamada M., Tabata S.; Kato M., Watanabe A., Watanabe A., Wanada M., Tabata S.; Kato M., Matanabe A., Watanabe A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute.

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X MEDLINE-94292520; PubMed-8021267;
Zhang S.-H., Broome M.A., Lawton M.A., Hunter T., Lamb C.J.;
Zhang S.-H., Broome M.A., Lawton M.A., Hunter T., Lamb C.J.;
Zhang S.-H., Broome M.A., Lawton M.A., Hunter T., Lamb C.J.;
Zhang S.-H., Broome M.A., Lawton M.A., Hunter T., Lamb C.J.;
T "AtpKl, a novel ribosomal protein kinase gene from Arabidopsis. II.
T "AtpKl, a novel plochemical analysis of the encoded protein.";
J. Biol. Chem. 269:17593(1994).
I. Diol. Chem. 269:17593(1994).
I. Diol. Chem. 269:17593(1994).
I. DEVELOPMENTE. Phosphorylates two ribosomal proteins, Pl4 and Pl6.
I. TISSUE SPECIFICITY: Expressed in all tissues.
I. Graving buds, root tips, leaf margins and germinating seeds.
In growing buds, root tips, leaf margins and germinating seeds.
I. PTM. Undergoes serine-specific autophosphorylation.
I. PTM. LAMILARITY: Belongs to the Ser/Thr family of protein kinases. S6
Kinase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

K->R: ACTIVITY SUBSTANTIALLY DIMINISHED.

407133D674CA271F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC10256; AAG51351.1; -.
PIR; 868462; S68462.
HSSP; Q63462; AAG51351.1; -.
InterPro; 1PR000961; Pkinase C.
InterPro; IPR000971; Prot kinase.
InterPro; IPR00371; Ser thr pkin AS.
InterPro; IPR00371; Ser thr pkin AS.
InterPro; IPR003290; Ser thr pkin AS.
InterPro; IPR00391; Pkinase. I.
Promom; PR00431; pkinase. I.
Promom; PR00431; pkinase. I.
PROSITE; PS001001; Prot kinase; I.
PROSITE; PS00107; PROTEIN KINASE ATP; I.
PROSITE; PS00108; PROTEIN KINASE ATP; I.
PROSITE; PS00108; PROTEIN KINASE ATP; I.
PROSITE; PS00108; PROTEIN KINASE DOM; I.
Transferase; Serine/threonine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
163
257
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163
257
257
163
465 AA;
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DOMAIN 134
NP_BIND 140
BINDING 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION
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                     189 IDHPPIVQLKYSFQTKYRLYLVLDFINGGHLFFQLYHQGLFREDLARVYTAEIVSAVSHL 248
                                                                                                                                                   197
                                                                                                                                                                       249 HEKGIMHRDLKPENILMDTDGHVMLTDFGLAKBFBENTRSNSMCGTTEYMAPBIV---RG 305
                                                                                                                                                                                                                                               LEHPFLVNLMYSPODEEDMFMVVDLLLGGDLRYHLQQNVHFKEBTVKLFICELVMALDYL 137
                                                                                                                                                                                                                             AGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKBIVHTFETTVVTYPSAWSQEMVSLL 257
VNPDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNEVRNVFKELQIMQG 77
                                                                                                                                                                                                                                                                                                    258 KKLLEPNPDOR----FSQLSDVQNFPYMNDINWDAVFQKRLIPGFIPNKGRLNCDPTFE 312
                                                                                                                                                                                                                                                                                                                            362 KGLLQKEPERRLGSGLSGAEEIKQHKWFKGINWKKLEAREVMPSFKPEVSGRQCIANFD 420
                                                                                                                                                   138 QNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPEMFSSRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Rad M.R., Xu G., Kirchrath L., Fritz C., Keuchel H., Hollenberg C.P.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen P.C., Lee K.S., Levin D.B.;
"A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell growth in Saccharomyces cerevisiae.";
Mol. Gen. Genet. 236:443-447(1993).
-i- FUNCTION: Plays an essential role in the proliferation of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. RAC SUBFAMILY. STRONGEST TO YPK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetacese; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation of a yeast protein kinase gene by screening with mammalian protein kinase cDNA.";
DNA 7:469-474(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1989 (Rel. 12, Created)
01-0CT-1984 (Rel. 29, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001ne-protein kinase YPK1 (BC 2.7.1.-).
YPK1 OR YK1126W.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 680 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISCUSSION OF SEQUENCE.
MEDLINE=93173125; PubMed=8437590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=89090805; PubMed=2850145;
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GO; GO:0005935; C:bud neck; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M21307; AAA34880.1; -. EMBL; Z28126; CAA81967.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z28126; CAA81967.1; -. PIR; S37955; S37955. HSSP; PO5132; LCTP. GermOnline, 139882; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maurer R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                    YPKI YEAST
ID YPKI YEAST
AC P12689;
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3;

Gaps

11;

Query Match 24.5%; Score 516.5; DB 1; Length 465; Best Local Similarity 34.1%; Pred. No. 2.9e-28; Matches 102; Conservative 66; Mismatches 120; Indels 11.

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452 AELLCALDNIHKLDVVYRDIKPENILLDVQGHIALCDFGLCKLNMKDDDKTDTFCGFPBY 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 TLAERTVLARVDCPFIVPLKPSFQSPEKLYFVLAPINGGELFYHLQKEGRFDLSRARFYT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 MAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTV---V 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 TYPSAWSQEMVSLLKKLLEPNPDQR--FSQLSDVQNPPYMNDINWDAVFQKRLIPGFIPN 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 KPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNEVRN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 KGRINCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHL-DSVQKEP 359
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GO; GO:0005829; C:cytosol; IDA.

GO; GO:0005886; C:plasma membrane; IDA.

R GO; GO:00064674; F:protein serine/threonine kinase activity; IMP.

R GO; GO:0006468; P:protein amino acid phosphorylation; IMP.

R GO; GO:0006665; P:sphingolipid metabolism; IMP.

R InterPro; IPR00091; Pkinase.

R InterPro; IPR00091; Pkinase.

R Fam; PR00433; Pkinase; I.

R PROSTIE; PR00107; PROTEIN KINASE ATP; I.

R RNOSITE; PS00107; PROTEIN KINASE DOM; I.

R PROSITE; PS00107; PROTEIN KINASE DOM; I.

R Transferase; Serine/threonine-protein kinase; ATP-binding.

FT TOWAIN 353 361 ATP (BY SIMILARITY).

R INDING 376 376 ATP (BY SIMILARITY).

R RINDING 376 176 II.

R RINDING 376 III.

R RINDING 376 III.

R RINDING 376 II.

R RINDING 376 II.

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ive 78; Mismatches 124; Indels
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STANDARD; PRT; 696 AA.
P50530; Q9UTP3;
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine-threonine-protein kinase sck1 (EC 2.7.1.37).
SCK1 OR SPACINS.02C.
Schizosaccharomyces pombe (Fission yeas).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycesales; Schizosaccharomycetes;
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MEDLINE=96120227; PubMed=7498728;
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                                                                                           DOR NO DO
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Menudrall, M., Pujita M., College B., Apolinatio B., Yamamoto M., Mundrall, a high copy number suppressor of defects in the cAMP-dependent proces, it also pathway in fisiant years, encodes a protein homologous for the Saccharomyces cerevisias SCH9 kinase.";

ENTRAINS-11849017 PabMed-1185356;
MENLINE-21849017 PabMed-1185356;
MENCINE-21849017 PabMed-1185356;
MENCINE M. MODIA K. MENDRALL M. MARCHE B., HANTE B., MECODE N. MENDRALL M. MARCHE B., MENDRAL B., MENDR
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                                                                                                                                                                                                                                                                                                                                                                  245 YP-SAWSQEMVSLLKKLLEPNPDQRFSQLSD---VQNFPYMNDINWDAVFQKRLIPGFIP 300
                                                                                                                                                                                                                                                                                   126 FICELVMALDYLQNQRIHRDMKPDNILLDEHGHVHITDFNIA-AMLPRETQITTMAGTK 184
                                                                                                                                                         11 VFDENEDVNF--DHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNEVRNV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TARC DROWE STANDARD; PRT; 352 AA.

RAPC DROWE STANDARD; PRT; 352 AA.

P12370; Q9V199;

01-0CT-1989 (Rel. 12, Created)

10-0K1-1990 (Rel. 42, Last sequence update)

10-0CT-2003 (Rel. 42, Last annotation update)

2AMP-dependent procein Kinase catalytic subunit (BC 2.7.1.37) (PKA C).

PKA-C1 OR CDKA OR DCO OR CG4379.

Drosophila melanogaster (Fruit fly).

Bukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adama M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.W.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kalderon D., Rubin G.M.;
"Isolation and characterization of Drosophila cAMP-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=88115281; PubMed=2828348;
FOSTET J.L., Higgins G.C., Jackson R.F.;
FOSTET S.L., Higgins G.C., Jackson R.F.;
FOIDING, sequence, and expression of the Drosophila cAMP-dependent protein kinase catalytic subunit gene.";
J. Biol. Chem. 263:1676-1681(1988).
                                                                                                                             15;
                                                                                              DB 1; Length 696;
                                                                                          24.3%; Score 511.5; DB 1; Length (36.9%; Pred. No. 1e-27; Live 63; Mismatches 112; Indels
                                            A -> R (IN REF. 1).
A7B05F5EE4D42AF7 CRC64;
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Canton-S;
MEDLINE=89107990; PubMed=3215511;
                                                              78594 MW;
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                                                                                                                           Conservative
308
331
428
199
199
696 AA;
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                                                                                                           Similarity
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                                                                                                                        Matches 111;
                               ACT SITE CONFLICT SEQUENCE
                                                                                          Query Match
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BINDING
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Man K.H. Doyle C., Baxter E., Halt C., Nella C., Salabatov S., Nella C., Carter A., Chanta I., Nella C., Nella C., Carter A., Chanta I., Nella C., Nella C., Nella C., Carter A., Chanta I., Nella C., Nella C., Nella C., Nella C., Nella C., Carter A., Chanta I., Nella C., Nella C., Nella C., Nella C., Carter A., Chanta I., Nella C., Nel
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J. Biol. Chem. 265:6896-6907(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKLFICELVMALDYLQNQ 140
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P21137; 018310; 018311;
01-MAY-1991 (Rel. 18, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CAMP-dependent protein kinase catalytic subunit (RC 2.7.1.37) (PKA C)
KIN-1 OR ZK909.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM B).
STRAIN=Bristol N2;
MEDLINE=90216721; PubMed=2324104;
Gross R.E., Bagchi S., Lu X., Rubin C.S.;
"Cloning, characterization, and expression of the gene for the catalytic subunit of cAMP-dependent protein kinase in Caenorhabditis elegans. Identification of highly conserved and unique isoforms generated by alternative splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
DR InterPro; IPR008271; Ser thr Dkin AS.

DR InterPro; IPR002296; Ser_thr_pkinase.

DR InterPro; IPR001245; Tyr Dkinase.

Brain, PF00069; pkinase.; 1.

DR PEAM; PF00069; pkinase.; 1.

DR PRINTS; PR00109; TYRKINASE.

DR PRINTS; PR00109; TYRKINASE.

DR SMART; SM00133; GTKZ; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

Transferase; Serine(threonine-protein kinase; ATP-binding; CAMP; M. Phosphorylation; Myristate; Lippopretein.

T ILIPPOT DEMONSITY.

DR PROSITE; PS00104; PROTEIN KINASE DOM; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                19; Gaps
                                                                                                                                                                                                                                           N-myristoyl glycine (By similarity).
PROTEIN KIMASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
SYSTALLARITY.
88542BCFA95E9640 CRC64;
                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 352;
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                                                                                                                                                                                                                                                                                                                                               Query Match 24.3%; Score 510.5; DB 1;
Best Local Similarity 34.4%; Pred. No. 5.5e-28;
Matches 110; Conservative 72; Mismatches 119;
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SEQUENCE
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isold=P21137-13; Sequence=VSP 004750, VSP 004758; SIMILARITY: Belongs to the Ser/\overline{T}hr family of protein kinases. cAMP
                                                                                                                                                                                              Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBUNIT: Composed of two regulatory chains and two catalytic
                                                                                                                                                                                                                                                                                                                                                Bvent=Alternative splicing; Named isoforms=13;
Comment=Experimental confirmation may be lacking for some
                                                         White S., McLay K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=a; Synonyms=Major;
IsoId=P21137-2; Sequence=VSP_004751, VSP_004758;
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IBOId=P21137-4; Sequence=VSP_004756, VSP_004757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P21137-12; Sequence=VSP_004758;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P21137-3; Sequence=VSP_004751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P21137-1; Sequence=Displayed;
                                                                                                                                              REVISIONS, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAS1610.1; JOINED.
AAAS1610.1; JOINED.
AAAS1610.1; JOINED.
AAAS1610.1; JOINED.
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EMBL; M37114; AAA51610.1; JOINED.
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CAD45614.1;
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CAD45616.1;
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CAD45618.1;
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                                                                                                                                                                                                                                                                                                                       -!- ALTERNATIVE PRODUCTS:
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SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                               lsoforms;
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                                                                                                                                                                                                                                                                                                  chains.
                                                                                                                                                                         Durbin R.;
Submitted
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VARSPLIC 1 53	VARSPLIC 1 53	FT VARSPLIC 1 53 MPTRLDITGNIQUEBOQRADVTACPVLPSPSSFS FT WASSPLIC 1 53 MPTRLDITGNIQUESSTPRGSMKERKNEALKNHKSK FT KLSILDDPVEDF -> MLSSSFFRGSMKERKNEALKNHKSK FT YIGGSYLETV (in isoform k).  FT VARSPLIC 1 72 MPTRLDITGNIQUEBODGADVTACPVLPSPSSFS FT KLSILDDPVEDFFKSFLDKAREDFKORMENPA -> MEREEW	RRRLSAAIRREDEGSLEEDEBEDEGFILHPLCR ASNSTTTITTPESSTTTTSPRNASSPENDES PELTTALSFPVALLSPRNTTSSITTGLVKKRR REKI PHILLKTSSGVVVPLASRGQRAPAITLC TVPPPSSSTFSVTSSLPFKTPNCGSKDDTDARS RQPTTSTSAPVSPIDHRQVRRGGRGVVPSGQV LKTQLSDRWSMKWLF (in isoform c) // FTId=VSP 004756	FIT VARSFLIC 348 404 ITPESFSNGSNGALFEALLIFYUGEADIRAFVED PET PT	NEDVNFDHFEILRAIGKGSFGBVCIVQKND: 	OY 71 BLQIMQQLEHPPLVNLWYSFQDBEDMFMVVDLLLGGDLRYHLQQNVHFKEBTVKLFICEL 130	Qy 131 VMALDYLONORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPE 190 	OY 191 MPSSRKGAGYSPAVDWMSLGVTAYBLEGRRPYHIRSSTSSKBIVHTFBTTVVTYPS 247	Qy 248 AWSQEMVSLLKGGLEPNPDQRF8QLSDVQNPPYMNDINWDAVFQKRLIPGFIPNKG 303	BSN—RSN—	KAPA_CRIGR STANDARD; PRT; 350 AA.  ID FAPA_CRIGR STANDARD;  AC P25321;  DT 01-MAY-1992 (Rel. 22, Created)  DT 01-MAY-1992 (Rel. 22, Last sequence update)  DT 01-GCT-2003 (Rel. 42, Last annotation update)  DE CAMP-dependent protein kinase, alpha-catalytic subunit (EC 2.7.1.37)  DB (PKA C-alpha).
EMBL, 282096; EMBL, 281511; EMBL, 282096; EMBL, 281511; EMBL, 281511; EMBL, 281511; EMBL, 282096; EMBL, 282096;	EMBL; 282096; EMBL; 281511; EMBL; 281511; EMBL; 282096; EMBL; 281511; EMBL; 282096; EMBL; 281511;		887.1; 887.1; 888.1; 889.1; 990.1;	PIR; A5.755; OKKWC PIR; R35755; OKKWC PIR; T21211; T2121 HSSP; P05132; T2121 WormPep; ZK909.28; WormPep; ZK909.28;	DR WormPep; ZK909.2d; CB31756.  DR WormPep; ZK909.2e; CB31757.  DR WormPep; ZK909.2f; CB31758.  DR WormPep; ZK909.2g; CB31759.	MormPep; ZK909.21; WormPep; ZK909.21; WormPep; ZK909.2j; WormPep; ZK909.2k;	WormPep; InterPro; InterPro; InterPro;	InterPro; IPR001245; Pfam; PF00069; pkina PRINTS; PR00109; TYR ProDom; PD000001; Px	DR SMART; SM00220; S_TKC; 1.  DR SMART; SM00219; TYTKC; 1.  DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.	Transferase, Serine/Chreenine-Protein Phosphorylation, Alternative splicing DOMAIN 81 335 PROTEIN NP BIND 87 95 ATP (BY BINDING 110 110 ATP (BY	FT ACT_SITE

PHOSPHORYLATION (BY SIMILARITY).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R InterPro; IPR000961; Pkinase C.
R InterPro; IPR000961; Pkinase C.
R InterPro; IPR00096271; Ser thr pkin AS.
R InterPro; IPR0002290; Ser thr pkin AS.
R InterPro; IPR001245; Tyr Dkinase.
R Pfam; PF00069; pkinase; 1.
R Pfam; PF000109; TYRKINASE.
R PRINTS; PR001109; TYRKINASE.
R RAINTS; PR001109; TYRKINASE.
R RAINTS; PR001109; TYRKINASE.
R RAMART; SM00120; STKC; 1.
R PROSITE; PS00107; PROTEIN KINASE ATP; 1.
R PROSITE; PS00117; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

RINZYME REGULATION: Activated by CAMP.

SUBUNIT: A number of inactive tertameric holoenzymes are produced by the combination of homo- or heterodimers of the different regulatory subunits associated with two catalytic subunits. CAMP causes the dissociation of the inactive holoenzyme into a dimer of regulatory subunits bound to four CAMP and two free monomeric catalytic subunits.

SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and
                                                                                                                                       SEGUENCE FROM N.A.
MEDLINE-91244783; PubMed-1645343;
Howard P., Day K.H., Kim K.E., Richardson J., Thomas J., Abraham I.,
Fleischmann R.D., Gottesman M.M., Maurer R.A.;
"Decreased catalytic subunit mRNA levels and altered catalytic subunit mRNA levels and catalytic subunit mRNA sevels and catalytic subunit mRNA sevels and structure in a cAMP-resistant Chinese hamster ovary cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

N-myristcyl glycine (By similarity).
DEAMIDATION (PRRIAL) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monomeric catalytic subunit). Translocates into the mucleus (monomeric catalytic subunit) (By similarity). TISSUE SPECIFICITY: Ubiquitously expressed in mammalian tissues. PTM: Asn-2 is partially deaminated to Asp-2 giving rise to 2 major isoelectric variants, called CB and CA respectively (By
                   Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SIMIGARITY: Belongs to the Ser/Thr family of protein kinases.
CAMP subfamily.
                                                                                                                                                                                                                                                                                  J. Biol. Chem. 266:10189-10195(1991).
-!- FUNCTION: Phosphorylates a large number of substrates in the cytoplasm and the nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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HSSP; P05132; 1CTP.
                                                                                               NCBI_TaxID=10029;
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                                                                                                                                                                                                                                                                                                                                                                                                             41 DHFDRIKTLGTGSFGRVMLVKHKETGNHYAMKILDKQKVVKLKQIBHTLNEKRILQAVNF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 RIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTWAGTKPYMAPEMFSSRKGAGY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 NKAVDWWALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGKVRFPSHFSSDLKDLL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 SFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTV---VTYPSAWSQEMVSLL 257
                                                                                                                                                                                                                                                                                                                                         21 DHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNEVRNVFKELQIMQGLEH 80
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MEDLINE=93183878; PubMed=8443157;
Zheng J., Knighton D.R., ten Byck L.F., Karlsson R., Xuong N.,
Taylor S.S., Sowadski J.M.,
"Crystal structure of the catalytic subunit of cAMP-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEANIDATION OF ASN-2, AND SUBCELLULAR LOCATION.
MEDLINE-20153511; PubMed-10684253;
Pepperkok R., Hotz-Wagenblatt A., Koenig N., Girod A., Bossemeyer D.,
                                                                                                                                                                                                                                                Indels 19; Gaps
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10-OCT-2003 (Rel. 42, Last annotation update)
CAMP-dependent protein kinase, alpha-catalytic subunit (EC 2.7.1.37)
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MEDLINE=87304251; PubMed=2441988;
Adavani S.R., Schwarz M., Showers M.O., Maurer R.A., Hemmings B.A.;
"Multiple mRNA species code for the catalytic subunit of the cAMP-dependent protein kinase from LLC-PK1 cells. Evidence for two forms of the catalytic subunit.";
Eur. J. Blochem. 167:221-226(1987).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Cetartiodactyla, Suina; Suidae; Sus.
1101 _ TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 KKLLEPNPDQRFSQL----SDVQNFPYMNDINWDAVPQKRLIPGFIPN-KG 303
                                                                                                                                                  Length 350;
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                                         40488 MW; 2EFC89F73A0DE53D CRC64;
                                                                                                                                             Query Match 23.9%; Score 502.5; DB 1; Best Local Similarity 34.0%; Pred. No. 1.9e-27; Matches 99; Conservative 76; Mismatches 97;
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338 3
350 AA;
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R InterPro; IPR000961; Pkinase C.
InterPro; IPR000951; Ser thr pkinase.
R InterPro; IPR000371; Ser thr pkinase.
R InterPro; IPR002291; Ser thr pkinase.
R Pfam; PF00431; pkinase C; 1.
R PF00431; pkinase C; 1.
R SMART; SM00133; S TK Z; 1.
R RPGSTTE; PS00108; PROTEIN KINASE ATP; 1.
R PROSTTE; PS00108; PROTEIN KINASE DM; 1.
R PROSTTE; PS0011; PROTEIN KINASE DM; 1.
              Blochemistry 32:2154-2161(1993).

-!- FUNCTION: Phosphorylates a large number of substrates in the cytoplasm and the nucleus.

-!- CATALYIC ACTIVITY: ATP 4 a protein = ADP + a phosphoprotein.

-!- CATALYIC ACTIVITY: ATP 4 a protein = ADP + a phosphoprotein.

-!- SUBUNIT: A number of inactive tetrameric holoenzymes are produced by the combination of homo- or heterodimers of the different regulatory subunits associated with two catalytic subunits. CAMP causes the dissociation of the inactive holoenzyme into a dimer of regulatory subunits bound to four CAMP and two free monomeric
                                                                                                                                                                                                                                                                   -1- SUBCELLUIAR LOCATION: Cytoplasmic (inactive holoenzyme and monomeric catalytic subunit). Translocates into the nucleus (monomeric catalytic subunit) (By similarity).
-1- TISSUE SPECIFICITY: Ubdquitously expressed in mammalian tissues.
-1- TISSUE SPECIFICITY: Ubdquitously of my and of the bander of the specific metal pammers.
-1- TISSUE SPECIFICITY: Ubdquitously langer nuclear/cytoplasmic ratio than the
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PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asp-2 form. Salongs to the Ser/Thr family of protein kinases.
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CLOSE TO OR AT THE PEPTIDE SUBSTRATE
BINDING SITE.
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complexed with MgATP and peptide inhibitor.";
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DEAMIDATION (PARTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X07617; CAA30470.1; -.
                                                                                                                                                                                                                                                       catalytic subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAMP subfamily.
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                       99 NPPFLVKLEYSFKONSNLYMVMEYVPGGEMFSHLRRIGRFSEPHARFYAAQIVLTFEYLH 158
                                                                                                                                                               GYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTV---VTYPSAWSQEMVS 255
                                                                                                                                                                                        79 BHPFLVNLWYSFQDEEDMFWVDLLLGGDLRYHLQQNVHFKEETVKLFICELVMALDYLQ 138
                                                                             139 NORITHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTWAGTKPYMAPEMFSSRKGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 265:2077-2082(1994).

-!- FUNCTION: Protein kinase that is part of growth control pathway which is at least partially redundant with the cAMP pathway.

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-!- ENZYME REGILATION: Activated by CAMP.

-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP.
                                                                                                       Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis B., Menezes S., Mouser L., Nan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Milcox L., Mohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             di Blasi F., Carra B., de Vendittis B., Masturzo P., Burderi E.,
Lambrinoudaki I., Mirisola M.G., Seidita G., Pasano O.,
"The SCH9 protein kinase mRNA contains a long 5' leader with a small
open reading frame.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-882255839; PubMed=3290050;
Toda I., Cameron S., Sass P., Wigler M.;
"SCH9, a gene of Saccharomyces cerevisiae that encodes a protein
distinct from, but functionally and structurally related to, CAMP-
dependent protein kinase catalytic subunits.";
Genes Dev. 2:517-527(1988).
                                                                                                                                                                                                                                                                      268 LLRNLLQVDLTKRFGNLKNGVNDIKNHKWFATTDWIAIYQRKVBAPPIPKFKG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                256 LLKKLLEPNPDORFSQL----SDVQNFPYMNDINWDAVFQKRLIPGFIPN-KG
                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1989 (Rel. 12, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Serinc/chreonine-protein kinase SCH9 (EC 2.7.1.37).
SCH9 OR KOMI OR YHR205W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=JR26-19D;
MEDLINE-93182531; PubMed=8442384;
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MEDLINE=94378003; PubMed=8091229;
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P11792;
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SCH9_YEAST
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Gaps

19;

23.9%; Score 502.5; DB 1; Length 350; 34.1%; Pred. No. 1.9e-27; ive 75; Mismatches 99; Indels 19

Best Local Similarity 34.1 Matches 100; Conservative

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 IA-AMLPRETQITTMAGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVTAYBLLRGRRPYHI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMKYMNKQKCVERNEVRNVFKELQIM----QGLEHPFLVNLWYSFQDEEDMFMVVDLLLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 RSSTSSKEIVHTFETTVVTYP-SAWSQEMVSLLKRLLEPNPDQRFSQLSD---VQNFPYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 --AENNOKMYQKIAFGKVKFPRDVLSQEGRSFVKGLINRNPKHRLGAIDDGRELRAHPFF
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                                                                                                                                                                              GO; GO:0004674; F:protein serine/threonine kinase activity, IGI. GO; GO:0007574; P:cell aging (sensus Saccharomyces); IMP. GO; GO:0006468; P:protein amino acid phosphorylation; IGI. GO; GO:0008361; P:regulation of cell size; IDA.
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ASN-RICH.
670 C2 DOMAIN.
670 PROTEIN KINASE.
425 ATP (BY SIMILARITY).
674 ATP (BY SIMILARITY).
675 BY SIMILARITY).
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N -> K (IN REF. 1).
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Pram; PROOL69; pkinase; 1.
Probom; PROOL69; pkinase; 1.
Probom; PROOL3; pkinase; 1.
SWART; SMO0239; C2; 1.
SWART; SMO0133; STKX; 1.
PROSITE; PSO0107; PROTEIN KINASE ATP; 1.
PROSITE; PSSO0104; PROTEIN KINASE DOM; 1.
PROSITE; PSSO011; PROTEIN KINASE DOM; 1.
PROSITE; PSSO004; C2, DOMAĪN_2; FĀLSE_NEG.
                                                                                                                                                                                                                                      InterPro; IPR000008; C2.
InterPro; IPR008973; C2 CalB.
InterPro; IPR008973; PkInase.
InterPro; IPR00951; PkInase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR0082790; Ser_thr_pkin_AS.
                                                                       EMBL; X12560; CAA31073.1; -.
EMBL; X57629; CAA40853.1; ALT_INIT.
EMBL; U00029; AAB69735.1; -.
PIR; S48986; S48986.
HSSP; P05132; 1FMO.
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750 N
91680 MW;
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                                                                                                                                                  GermOnline; 139523; -. SGD; S0001248; SCH9.
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823 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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-!- DISEABE: Defects in RPS6KA3 are the cause of Coffin-Lowry syndrome (CLS) [MIM:03600], an X-linked dominant disorder characterized by severe mental retardation with facial and digital dysmorphisms, and progressive skeletal deformations.
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Novel mutations in Rsk-2, the gene for Coffin-Lowry syndrome (CLS).";

    Bur. J. Hum. Genet. 7:20-26(1999).
    -1- FUNCTION: Phosphorylates a wide range of substrates including ribosomal protein S6. Implicated in the activation of the mitogenactivated kinase cascade.
    -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
    -1- TISSUR SPECIFICITY: Expressed in many tissues, highest levels in

                                                                         01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 42, Last sequence update)
10-0cT-2003 (Rel. 42, Last amnotation update)
Ribosomal protein S6 kinase alpha 3 (EC 2.7.1.37) (86K-alpha 3) (90
RDa ribosomal protein S6 kinase 3) (p90-RSK 3) (Ribosomal S6 kinase 2)
(RSK-2) (pp90RSK2) (Insulin-stimulated protein kinase 1) (ISPK-1).
RPS6KA3 OR RSK2 OR ISPK1.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUR=Placenta, and T-cell;
MEDLINE=95113120; PubMed=7813820;
MEDLINE=95113120; PubMed=7813820;
MEDLINE=95113120; PubMed=7813820;
Yang P.Y., Vestergaard H., Richmond K., Hansen T., Erikson R.L.,
Miklos G.L.G., Cohen P.T.W., Pedersen O.;
"Cloning of a human insulin-stimulated protein kinase (ISPK-1) gene
and analysis of coding regions and mRNA levels of the ISPK-1 and the
protein phosphates-1 genes in muscle from NIDDM patients.";
Diabetes 44:90-97(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Skaletal muscle;
MEDLINE-94189676; PubMed-8141249;
Moller D.E., Xia C.-H., Tang W., Zhu A.X., Jakubowski M.;
"Human rsk isoforms: cloning and characterization of tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jacquot S., Merienne K., de Cesare D., Pannetier S., Mandel J.-L., Sassone-Corsi P., Hanauer A.; "Mutation analysis of the RSK2 gene in Coffin-Lowry patients: extensive allelic heterogeneity and a high rate of De novo
                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MARIANTS CLS PHE-82; GLN-127; TYR-154; VAL-225 AND ASP-431, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS CLS VAL-75 AND ALA-227.
MEDLINE-97111410; PubMed-8955270;
Trivier B., de Cesare D., Jacquot S., Pannetier S., Zackai F.
Trivier B., Mandel J.-L., Sassone-Corsi P., Hanauer A.;
"Mutations in the kinase Rek-2 associated with Coffin-Lowry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS CLS TRP-114 AND GLN-729.
WIRDLINES-19191975; PubMed=10094187;
Abidi F., Jacquot S., Lassiter C., Trivier B., Hanauer A., Schwartz C.E.;
                                    740 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Am. J. Hum. Genet. 63:1631-1640(1998).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression.";
Am. J. Physiol. 266:C351-C359(1994)
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT SER-38.
MEDLINE-99057500; PubMed-9837815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 2-582 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vature 384:567-570(1996).
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinase subfamily.
                                                                                                                                                                                                                          (Human)
                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutations."
                                    K6A3_HUMAN
RESULT 13
K6A3_HUMAN
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56 VKEGHEKADPSQPELLKVLGQGSPGKVFLVKKISGSDARQLYAMKVLKKATLKVRDRVRT 115

116 KM-ERDILVEVNHPPIVKLHYARQTEGKLYLILDFLRGGDLFTRLSKEVMFTEBDVKFYL 128 CELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIA-AMLPRETQITTMAGTKPY 187 MAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVVTYP

> ઠ 셤 8 셤 ò 셤 8

69 VFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEBTVKLFI

186 234 246

174

||||: : | |: : |||| || :|: | || || 235 MAPEVVINRR---GHIQSADWWSFGVLMFEMLTGTLPF---QGKDRKETMIMILKAKLGMP 288 247 SAWSQEMVSLLKKILEPNPDQRFSQ----LSDVQNFPYMNDINWDAVFQKRLIPGFIPNK 302 289 QFLSPEAQSLLRMLFKRNPANRLGAGPDGVEEIKRHSFFSTIDWNKLYRREIHPPFKPAT 348

GR----LNCDPTF 311 349 GRPEDTFYFDPEF 361

303

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                                                                                                                                                                                           Min; 303600; -.

R GO; GO:0004614; F:protein serine/threonine kinase activity; TAS.

R GO; GO:0007165; P:signal transduction; TAS.

R GO; GO:0007165; P:signal transduction; TAS.

R GO; GO:0001501; P:skeletal development; TAS.

R GO; GO:0001501; P:skeletal development; TAS.

R InterPro; IPR000961; Prinase C.

InterPro; IPR000271; Ser Ehr Dkinase.

R InterPro; IPR001290; Ser Lhr Dkinase.

R InterPro; IPR001290; Ser Lhr Dkinase.

R InterPro; IPR001290; Ser Lhr Dkinase.

R InterPro; IPR00109; TRXINASE.

R PROMO 13; PROTEIN KINASE ATP; 2.

R SWART; SW00130; PROTEIN KINASE ATP; 2.

R ROSITE; PS001001; PROTEIN KINASE ST; 2.

R PROSITE; PS001001; PROTEIN KINASE ST; 2.

R PROSITE; PS001001; PROTEIN KINASE DOM; 2.

R TRANSGEASE, SERING-CHROMING; PROTEIN KINASE ST; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.8%; Score 501.5; DB 1; Length 740; 35.1%; Pred. No. 5.4e-27; tive 66; Mismatches 118; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Multigene family; Disease mutation; Polymorphism. DOMAIN 68 327 PROTEIN KINASE 1. DOMAIN 422 679 PROTEIN KINASE 2. NP BIND 74 82 ATP (BY SIMILARITY). BINDING 100 100 ATP (BY SIMILARITY). ATCT SITE 193 193 BY SIMILARITY. NP BIND 451 451 ATP (BY SIMILARITY).
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486AE8357CEAB6C8 CRC64;
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D -> Y (IN CLS).

PTId='VAR_006193.

A -> V (IN CLS).

/PTId='VAR_006194.

S -> A (IN CLS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR 006195.

G \rightarrow D (I\overline{N} CLS).

/FTId=VAR 006196.

R \rightarrow Q (I\overline{N} CLS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR 006197.
V -> L (IN REF. 2)
K -> N (IN REF. 2)
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G -> V (IN CLS).
/FTIG=VAR 006189.
V -> F (IN CLS).
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                                                                                              EMBL; U08316; AAA81952.1; -.
EMBL; L07599; AAC82495.1; -.
PIR; I38956; I38556.
HSSP; Q63450; IA06.
Genew; HGNC:10432; RPS6KA3.
MIM; 300075; -.
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740 AA;
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CONFLICT
SEQUENCE
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ACT SITE
VARIANT
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K6A3 MOUSE STANDARD; PRT; 740 AA.
P18654; Q03140; QBK3J8;
01-NOV-1990 (Rel. 16, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kibosomal protein S6 kinase alpha 3 (EC 2.7.1.37) (S6K-alpha 3) (90
kDa ribosomal protein S6 kinase alpha (P90-RSK 3) (Ribosomal S6 kinase 2)
(RSK-2) (pp90RSK2) (MAP kinase-activated protein kinase 1b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
--- TISSUB SPECIFICITY: Intestine, thymus, lung, heart and brain.
--- PTM: Autophosphorylated on Ser-386, as part of the activation process (By similarity).
--- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6
                                                                                                                                                                                                     SEQUENCE FROM N.A. PubMed=12016217; Chrestensen C.A., Sturgill T.W.; Chrestensen C.A., Sturgill T.W.; "Characterization of the p90 ribosomal 86 kinase 2 carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                      [2]
SEQUENCE OF 108-740 FROM N.A.
MEDLINE=89384612; PubMed=2779569;
Alcorta D.A., Crews C.M., Sweet L.J., Bankston L., Jones S.W.,
Erikson R.L.;
                                                                                                                                                                                                                                                         domain as a protein kinase.";
J. Biol. Chem. 277:27733-27741(2002)
                                                                                                                          RPS6KA3 OR RSK2 OR RPS6KA-RS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinase subfamily.
                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                             (MAPKAPK1B)
     Gaps
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Best Local Similarity 35.19 Matches 110; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 QFLSPEAGSLLRMLFKRNPANRLGAGPDGVEEIKRHSFFSTIDWNKLYRREIHPPFKPAT 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VFKELQIMQGLEHPFLVNLWYSFQDEEDMFWVVDLLLGGDLRYHLQQNVHFKEETVKLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 CELVMALDYLONORIIHRDMKPDNILLDEHGHVHITDFNIA-AMLPRETQITTMAGTXPY
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35.1%; Pred. No. 5.4e-27;
tive 66; Mismatches 118; Indels 19; Gaps
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PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:104557; Rps6ka3.
GO; GO:0004674; P:protein serine/threonine kinase activity; IDA
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR00091; Pkinase C.
InterPro; IPR00091; Pkinase C.
InterPro; IPR00021; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
IPfam; PP00403; pkinase; 2.
IPFAM; PR00109; TYRKINASE.
IPR051TB; PS00100; TYRK; 1.
IPR051TB; PS00107; PROTEIN KINASE ATP; 2.
IPR051TB; PS001109; PROTEIN KINASE ST; 2.
IPR051TB; PS001109; PROTEIN KINASE ST; 2.
IPR051TB; PS001109; PROTEIN KINASE DOM; 2.
IPR051TB; PS001109; PR07EIN KINASE DOM; 2.
IPR051TB; PS001109; PP07EIN KINASE DOM; 2.
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PHOSPHORYLATION (BY SIMILARITY)
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PROTEIN KINASE 2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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DOMAIN 68 327 PROTEIN KINAS.
NP MAIN 74 22 679 PROTEIN KINAS.
NP BIND 74 82 ATP (BY SIMILARITY ACT SITE 193 193 BY SIMILARITY APPENDEN.
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PIR; S30504; S30504.
HSSP; Q63450; 1A06.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content. is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=93173125; PubMed=8437590;
Chen P.C., Lee K.S., Levin D.E.;
The pair of putative protein kinase genes (YPK1 and YPK2) is required for cell growth in Saccharomyces cerevisiae.";
Mol. Gen. Genet. 236:443-447(1993).
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SEQUENCE FROM N.A.
MEDLINE=97313268; AB972;
MEDLINE=97313268; PubMed=9169872;
BOWMAN S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Huut S.,
Connor R., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.
Rice P., Skelton J., Walsh S., Whitchead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-CCT-2000 (Rel. 42, Last sequence update)
10-CCT-2001 (Rel. 42, Last annotation update)
10-CCT-2001 (Rel. 42, Last annotation update)
10-CST-2001 (Rel. 42, Last annotation update)
10-KR2 OR YKR2 (Rel. 42, Last annotation update)
10-KR2 OR YKR2 (Rel. 42, Last annotation update)
10-KR2 OR YKR2 OR YKR104C OR YM9718 (D3C
10-KR2 OR YKR2 OR YKR104C OR YM9718 (D3C
10-KR2 OR YKR2 OR YKR2 (Rel. 42, Last annotation)
10-KR2 OR YKR2 OR YKR2 OR YM9718 (D3C
10-KR2 OR YKR2 OR YKR2 OR YM9718 (D3C
10-KR2 
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InterPro; IPR000719; Prot_kinase_C.
InterPro; IPR000719; Prot_kinase_C.
InterPro; IPR0008271; Ser_thr_pkinase.
InterPro; IPR000590; Ser_thr_pkinase.
InterPro; IPR000590; Ser_thr_pkinase.
InterPro; IPR0005001; Prot_kinase_C: 1.
InterPro; IPR000131; INTERIOR INTERIO
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MEDLINE=89306654; PubMed=2663649;
MEDLINE=89306654; PubMed=2663649;
MED K., Ohno S., Matsumoto S., Yahara I., Suzuki K.;
"A novel yeast gene coding for a putative protein kinase.";
Gene 76:177-180(1989).
                                                                              677 AA
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PROTEIN KINASE
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                                                                              PRT;
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EMBL; Z49702; CAA89740.1; -.
PIR; JS0178; JS0178.
GermOnline; 142772; -.
SGD; S0004710; YPKZ.
GO; GO:0005737; C:Cycoplasm; IDA.
GO; GO:0005734; C:nucleus; IDA.
                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                  YEAST
RESULT 15
YPK2 YEAST
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128 CELVMALDYLONQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQIT-TWAGTKPY 186
                                                                                                                                                                                                                                                      508
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                                                                                                                                                                                     389 TLAERTVIARVDCPFIVPLKFSPQSPEKLYLVIAFINGGELFYHLQHEGRFSLARSRFYI 448
                                                                                                                                                                                                                                                                                                                               246 PSAWSQEMVSLLKKLLEPNPDQRF--SQLSDVQNPPYMNDINWDAVFQKRLIPGFIPNKG 303
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                                                                                           Gaps
                                                              Query Match 23.8%; Score 501; DB 1; Length 677; Best Local Similarity 32.5%; Pred. No. 5.2e-27; Matches 116; Conservative 76; Mismatches 127; Indels 38;
358 ATP (BY SIMILARITY).
373 ATP (BY SIMILARITY).
467 BY SIMILARITY.
76664 MW; BIPAB0295386A113 CRC64;
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350 3
373 3
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NP BIND
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 25, 2004, 10:46:29; Search time 21 Seconds (without alignments) 1813.897 Million cell updates/sec Run on:

US-10-667-442-2 2104 1 MGANTSRKPPVFDENEDVNF......NLALEQTKDPQGEDGQNNNL 396 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	protein kinase 2 (	protein kinase (BC	(1)	protein kinase ATP		kinase	kinase	protein kinase ATP		hypothetical prote	hypothetical prote	hypothetical prote	protein kinase (EC	probable protein k	protein kinase (EC	ribosomal protein	protein kinase YKR	al protei	kinase	kinase	kinase	protein kinase (BC	kinase	kinase	protein kinase (EC		kinase	
SUMMARIES	ID	}	A38578		856639										OKHYCA	: S48986	_						. OKRT2C	_	. OKRTCB	OKMSCB	OKHYCB	S19028	_	2 A53758
	Length DB							696 2							351 1	823 2		•	•		359 1									
de	Query Match L	40.1	25.5	25.1	٠	24.5	•	24.3	24.3	24.1	24.1	24.1	24.0	23.9	23.9	m	23.8	23.8	23.8	23.8	23.7	23.7	3	23.6	23.6	23.6	ë.	-	23.6	23.6
	Score	84	537	528.5	521	516.5	513	511.5	510.5	508	507	506.5	206	503	502.5	502.5	501.5	501.5	501	500.5	499	498.5	98	496.5	496	496	496	496	9	495.5
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protein kinase C (	beta-adrenergic-re	ribosomal protein	cyclic adenosine 3	protein kinase (EC	probable serine/th	beta-adrenergic-re	protein kinase (BC	beta-adrenergic-re	protein kinase C-r	ribosomal protein	protein kinase (BC	protein kinase (EC	ribosomal protein	protein kinase (EC	protein kinase (BC
A49509	A53791	A32571	JC7968	OKBYC3	T38171	A40088	OKWISCA	156531	T28666	B30001	A60543	A54400	A30001	OKBYC2	окнисв
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495.5	495.5	494.5	493.5	493.5	493.5	493.5	492.5	492.5	492.5	491.5	490	490	488.5	487	486.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

PRESULT 1  T2368  hypothetical protein M03C11.1 - Caenorhabditis elegans  C, Species Caenorhabditis elegans  R, Accession: T23688  A, Accession: T2368  A, Accession: T23688  A, Accession: T2368  A, Accession: T2368  A, Accession: T2368  A, Accession: T2377  A, Anthriborycologion: T2468  A, Accession: T2468  A, Accession: T2468  A, Accession:
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RESULT 2 A38578

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Query Match
Best Local Similarity
Matches 107; Conserv
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C;Species: Dictyostellum discoideum
C;Species: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Apr-1998
C;Accession: JQ1150
R;Buerki, E.; Anjard, C.; Scholder, J.C.; Reymond, C.D.
Gene 102, 57-65, 1991
A;Title: Isolation of two genes encoding putative protein kinases regulated during Dicty A;Reference number: JQ1150; MUID:91323730; PMID:1864510
A;Accession: JQ1150
A;Accession: JQ1150
A;Residues: 1-648 eBUE>
A;Cross-references: GB:M38703
protein kinase 2 (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 24-Sep-1999
C;Accession: A38578
R;Haribabu, B.; Dottin, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum A;Reference number: A38578; MUD: 9142122; PMID: 1996312
A;Accession: A38578
A;Goccule type: DNA
A;Molecule type: DNA
A;Residues: 1-479 c.HAR>
A;Coss-references: GB: NS9744; NID: g167717; PIDN: AAA33186.1; PID: g167718
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase homolo C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase homolo F;Superfamily: protein kinase homology: RXIN>
F;159-167/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 SPEAKSLLEGLLTREVDKRLGTKGGGEVKOHPWFKNIDWEKLDRKEVEVHFKPKVKSGTD 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 KELQIMQGLEHPFLVNLWYSFQDBEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKLFICE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQEMVSLLKKLLEPNPDQRFSQL--SDVQNFPYMNDINWDAVFQKRLIPGFIP----NKG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMPSSRKGAGYSPAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTPETTVVTYPSAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VPDBN-EDVNPDHPEILRAIGKGSPGEVCIVQKNDTKKMCAMKYMNKQKCVERNEVRNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                             25.5%; Score 537; DB 2; Length 47 36.2%; Pred. No. 2.4e-17; Live 66; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 ISQIDPVFTQERPMDSLVETSAL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 RINCOPTFELE --- EMILESKPL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 36.2
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 578/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130
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A; Residues: 1-480 <hUT>
A; Residues: 1-480 <hUT>
A; Cross-references: EMBL: X79992; NID: 9871985; PIDN: CAA56313.1; PID: 9871986
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
C; Keywords: ATP; phosphotransferase; protein kinase
F;149-407/Domain: protein kinase homology <kIN>
P;157-165/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              two kinases that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKRIVHTFETTVVTYPSAWSQEM 253
                                                                                                                                                                                                                                                                                                           325 PPV---NARERLKEFKQIRVLGTGTFGKVYLIQ--NTKDGCYYAMKCLNKAYVVQLKQVE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                               439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAMSQEMVSLLKKLLEPNPDQRFSQLS----DVQNFPYMNDINWDAVFQKRLIPGFIPNK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 IMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHPKEBTVKLFICELVMA 133
                                                                                                                                                                                                                                                                     99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tibosomal protein S6 kinase homolog (clone Aspkil) - oat
NiAlternate names: mitogen-activated protein kinase pp70 homolog
Cispecies: Avena sativa (oat)
Cispecies: Avena sativa (oat)
Cispecies: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
Cispecies: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
Cispecies: S56cession S56c39
Filtitly, A.K., Phillips, A.L.
Plant Mol. Biol. 27, 1043-1052, 1995
A/Filte: Gibberallin-regulated expression in oat aleurone cells of two kinase A/Reference number: S56c38; MUID:95284341; PMID:7766874
                                                                                                                                                                                                                                                                                                                                                                                                 67 NVFKELQIMQGLEHPFLVNLWYSFQDEEDMFWVDLLLGGDLRYHLQQNVHFKEETVKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||: |: |: |||||||||: :|:| | |:: |:|
498 LAPEIIQSK---GHGKAVDWWALGILIFEMLAGYPPFY---DDDTFAIYNKILAGRITFP
                                                                                                                                                                                                                                                                     9 PPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMC--AMKYMNKQKCVERNEVR
                                                                                                                                                                                                                                                                                                                                                                                                                                   380 HINSEKSILSSIHHPPIVNLYQARQDEKKLYLLFBYVAGGEVFTHLRKSMKFSNSTAKFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 MAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVVTYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 ICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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F;342-350/Region: protein kinase ATP-binding motif
F;365,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted
F;464,468/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                  Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Mismatches 124; Indels
                                                                                                                                         DB 1;
                                                                                                                                                                 34.2%; Pred. No. ,... _... cive 76; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.8%; Score 521; DB 2; 35.3%; Pred. No. 1.2e-16;
                                                                                                                                      Score 528.5;
Pred. No. 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: nucleic acid sequence not shown
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QHQGDSSNFEMYDEERMVEEPP 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 GRLNCDPTFEL--EEMILESKP 322
                                                                                                                                         25.1%; Score
                                                                                                                                                                 Best Local Similarity 34.24
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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A; Residues: 1-680 - RAMS
A; Cross-references: EMBL: 228126; NID: 9486212; PIDN: CAA81967.1; PID: 9486213; MIPS: YKL12
A; Cross-references: EMBL: 228126; NID: 9486212; PIDN: CAA81967.1; PID: 9486213; MIPS: YKL12
B; Experimental source: strain $288C
B; Maurer, R.A.
DNA 7, 469-474, 1988
A; Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein A; Reference number: A31248; MUID: 89908065; PMID: 2850145
A; Recession: A31248
A; Recession: A31248
A; Residues: 1-200, 'L', 202-552, I', 554-680 - MAU>
A; Residues: 1-200, 'L', 202-552, I', 554-680 - MAU>
A; Residues: 1-200, 'L', 202-552, I', 554-680 - MAU>
A; Cross-references: EMBL: MID: 93172180; PIDN: AA34880.1; PID: 9172181
A; Cross-references: EMBL: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell A; Reference number: $30903; MUID: 93173125; PMID: 8437590
A; Recession: $30903; MUID: 93173125; PMID: 9437590
A; Recession: S30903
A; Recession: S30903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: SGD:S0001609; MIPS:YKL126w
A,Map position: 11L
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homo
C;Xeywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;345-602/Domain: protein kinase homology «KIN»
F;353-361/Region: protein kinase ATP-binding motif
F;470/Active site: ASp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K.; Hoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAMP-dependent - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein kinase (EC 2.7.1.37) sckl, cAMP-dependent - fission yeast (Schizosaccharomyces protein Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Species: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Nov-2000 C; Dates 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Nov-2000 C; Accession: S55694; T38040 B.M.; Apolinario, B.; Yamamoto, M.; Maundrell, K.; Hoff Genetics 140, 457-467, 1995 A; A; Tille: Schi, a high copy number suppressor of defects in the cAMP-dependent protein A; Reference number: S55694; MUID:96120227; PMID:7498728
          C. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
R;Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, submitted to the Protein Sequence Database, March 1994 A;Reference number: 837953 A;Accession: 837955 A;Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 VPKELQIMQGLEHPFLVNLWYSPQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEBTVKLFI 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563 VPPDGFDRDAKOLLIGILISRDPTRRIGYNGADBIRNHPPFSQLSWKRLLMKGYIPPYKPA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 TYPSAWSQEMYSLLKKLLEPNPDQR--FSQLSDVQNFPYWNDINWDAVFQKRLIPGFIPN 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 KPPVFDENEDVNFDHFELLRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNEVRN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGRINCDPTFELERMILESKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHL-DSVQKEP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 TLAERTVILARVDCPPIVPLKFSFQSPEKLYFVLAFINGGELFYHLQKEGRFDLSRARFYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELVMALDYLQNQRITHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQIT-TWAGTKPY
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24.4%; Score 513; DB 2; Length 680
Best Local Similarity 32.0%; Pred. No. 3.8e-16;
Matches 115; Conservative 78; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Reaidues: 1-200,'L',202-226,'T',228-552,'I',554-680 <CHE>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Gene: SGD: YPK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128
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A; Residues: 17465 < 2HA>
A; Cross-references: GB:L29030; NID:9508307; PIDN:AAA21142.1; PID:9508308
A; Cross-references: GB:L29030; NID:9508307; PIDN:AAA21142.1; PID:9508308
A; Note: sequence extracted from NCBI backbone (NCBIN:149344, NCBIP:149415)
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology C, Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F; 132-389/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-465 <MIZ.
A; Residues: 1-465 <MIZ.
A; Cross-references: EMBL: D42056; NID:9867996; PIDN:BAA07656.1; PID:d1008238; PID:9867997
A; Cross-references: EMBL: D42056; NID:9849
B; Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
A; Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
A; Title: atpkl, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation, Ch
A; Reference number: A54141; MUID:94292519; PMID:7912697
A; Contents: ecotype Landsberg erecta
A; Accession: A54141
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                  protein kinase ATPK6/ATPK1 (EC 2.7.1.-) - Arabidopsis thaliana ($5pecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C;Accession: 568462; A54141
R;Mizoquchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A;Title: Two genes that encode ribosomal-protein 56 kinase homologs are induced by cold A;Reference number: $68462; MUID:95129712; FMID:7828736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 IDHPFIVQLKYSFQTKYRLYLVLDFINGGHLFFQLYHQGLFRBDLARVYTABIVSAVSHL 248
                                                                                     376 HSLLKGLLHKEAGKRLGSGLGGSDEIXONHKWFKAVNWKRLEARQIQPSFCPNVAGQTCIA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 LEHPFLVNLMYSPQDEEDMPMVVDLLLGGDLRYHLQQNVHFKEETVKLPICELVMALDYL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 QNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTWAGTKFYMAPEMFSSRKG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 HEKGIMHRDLKPENILMDTDGHVMLTDFGLAKEFEENTRSNSMCGTTEYMAPEIV---RG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVVTYPSAWSQEMVSLL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVERNEVRNVFKELQIMQG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase YPK1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKL126w
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 24-Sep-1999
C;Accession: S37955; A31248; S30903
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                                                VSLLKKI,LEPNPDQRFSQ----LSDVQNFPYMNDINWDAVFQKRLIPGFIPNKGRLNCDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 516.5; DB 2;
Pred. No. 1.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.5%;
34.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                           TPE 312
                                                                                                                                                                                                                                            436 NPD 438
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A Gene: FlyBase: Pka-Cl
A; Gross-references: FlyBase: FB90000273
A; Cross-references: FlyBase: FB90000273
A; Cross-references: FlyBase: FB90000273
C; Superfamily: Kinase-related transforming protein; protein kinase homology
C; Superfamily: Arnase-related transforming; heterotetramer; lipoprotein; magnes.
C; Sa3/Product: protein kinase, CAMP-dependent, catalytic chain #status predicted 
F; 2-33/Product: protein kinase, AMP-dependent, catalytic chain #status predicted 
F; 2-60/Region: protein kinase ATP-binding motif F; 2-80, 124, 130, 173, 186/Binding site: Mg-Patry (Phe, Gly, Glu, Glu, Glu, Thr) #status predicted F; 171/Active site: Lys, Glu, App. Lys #status predicted F; 171/Active site: magnesium (Asn. Asp. Hastaus predicted F; 174, 187/Binding site: phosphate (Thr) (covalent) #status predicted F; 141/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-471 <MIZ>
A;Residues: 1-471 <MIZ>
A;Cross-references: BMBL:D42061; NID:g1526412; PIDN:BAA07661.1; PID:d1008243; PID:g86
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein kinase ATPK19 (BC 2.7.1.-) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: S64643
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FRBS Lett. 359, 199-204, 1995
A;Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by A;Reference number: 868462; MUID:95129712; PMID:7828736
                             A;Cross-references: GB:M18655; GB:J03504; NID:g157051; PIDN:AAA28412.1; PID:g157052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 KKLLEPNPDORPSQL----SDVQNPPYMNDINWDAVFQKRLIPGFIPN-KGRLNCDPTFB 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNILLOVDLTKRYGNIKAGVNDIKNOKWFASTDWIAIFOKKIEAPFIPRCKGPGDTSNFDD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 DHFBILRAIGKGSFGBVCIVQKNDTKKMCAMKYMNKQKCVERNBVRNVFKBLQIMQGLBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 DDFERIKTLGTGSFGRVMIVQHKPTKDYYAMKILDKQKVVKLKQVEHTLNBKRILQAIQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PFLVNLWYSPQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKLFICELVMALDYLQNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 RIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTWAGTKPYMAPBMFSSRKGAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 SPAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTV----VTYPSAWSQEMVSLL
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; Pred. No. 4.6e-16;
64; Mismatches 124; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.3%; Score 510.5; DB 2; Length 34.4%; Pred. No. 2.8e-16; tive 72; Mismatches 119; Indels
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Best Local Similarity 34.44
Matches 110; Conservative
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A;Residues: 2-353 <FOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP; phosphotransferase; protein kinase
F;300-563/Domain: protein kinase homology <KIN>
F;308-316/Region: protein kinase ATP-binding motif
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                                                                                                                    A;Cross-references: GB:D38108; NID:g1136301; PIDN:BAA07286.1; PID:d1007864; PID:g1136302
A)Note: the authors translated the codon GAT for residue 687 as His
R;McDougall, R.C.; Fajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase (EC 2.7.1.37), cAMP-dependent, catalytic chain - fruit fly (Drosophila protein kinase (EC 2.7.1.37), cAMP-dependent, catalytic chain - fruit fly (Drosophila C;Species: Drosophila melanogaster C;Date: 21.May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1999 R;Kalderon: C31751, A286.69 R;Kalderon: C31751, A286.69 R;Kalderon, D.; Rubin, G.M. Genes Dev. 2, 1539-1556, 1988 A;Title: Isolation and characterization of Drosophila cAMP-dependent protein kinase generate number: A31751; MUID:89107990; PMID:3215511
                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: EMB.Ail09951; PIDN:CAB53053.1; GSPDB:GN00066; SPDB:SPAC1B9.02c
A;Experimental source: strain 972h-; cosmid clB9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 FKELQIMQGL----EHPPLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 IGERNILVRISLDESPFIVGLKPSFOTASDLYLITDYMSGGELFWHLOHEGRFPEORAKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 696;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.3%; Score 511.5; DB 2; 36.9%; Pred. No. 4.5e-16; iive 63; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36.9
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: sckl; SPDB:SPAC1B9.02c
                                                                                                                                                                                                                                                A; Reference number: Z21764
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A; Residues: 1-353 < KAL>
                             Status: preliminary
Molecule type: DNA
Residues: 1-696 <JIN>
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                                                                                                                                                                                                                                                                             A;Accession: T38040
A;Status: prelimina
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A;Reference number: Z19241
A;Accession: T20232
A;Accession: T20232
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-785 cWIL>
A;Residues: 1-785 cWIL>
A;Residues: 1-785 cWIL>
A;Cross-references: RMBL:Z75533; PIDN:CAA99814.1; GSPDB:GN00019; CESP:C54G4.1
A;Reperimental source: clone C54G4
C;Genetics:
A;Gene: CESP:C54G4.1
A;Map position: 1
A;Map position: 1
A;Map position: 55/3; 188/2; 237/2; 339/3; 397/2; 474/3; 504/3; 558/2; 594/3; 687/1; 736/2
C;Superfamily: ribosomal protein $6$ kinase II; protein kinase homology
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R; White, S.
Rsubmitted to the EMBL Data Library, November 1996
A; Reference number: 220469
A; Reference number: 220469
A; Reference number: real to the RMBL Data Library and the real translated from GB/EMBL/DDBJ
A; Residence: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-359 cW12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL: 282096; PIDN:CAB05034.1; GSPDB:GN00019; CESP:ZK909.2a
A;Experimental source: clone ZK909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 KELQIMOGLE-HPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKLFIC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 PSAWSQEMVSLLKKLLEPNPDQR--FSQLSDVQNFPYMNDINWDAVFQKRLIPGFIPNKG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 PKTYMDVDARDFIGGLIEKKELEKRLGYNGVDEIKONHKFMSSIDWDAAVKRTLKPVIVPRIG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T21211; T28100
B;McLay, K.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19391
A;Recossion: T21211
A;Accession: T21211
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; Translated from T3201
A;Residues: DNA
A;Residues: DNA
A;Residues: T359 eWIL>
                                                  hypothetical protein C54G4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T20232
R;Wilkinson, J.
Submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:||: : :|||| ||||||||| ::||| | : : |||:|
188 MSPEVINRPEG-GYSDVVDWWSLGVISFELLTGCSPFTVDGAQNSSKDIAKRIMIKKVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 ENEDVNPDHPEILRAIGKGSFGEVCIVOK---NDTKKMCAMKYMNKOKCVERNE-VRNVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAPEMPSSRKGAGYSPAVDWWSLGVTAYELLRGRRPYHI-RSSTSSKEIVHTFETTVVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

24.1%; Score 506.5; DB 2; Length 'Best Local Similarity 36.3%; Pred. No. 8.4e-16;
Matches 109; Conservative 73; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:ZK909.2a
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C;Species: Aplysia californica (california sea hare)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Jun-1999
C;Accession: S19027
R;Beushausen, S.; Bergold, P.; Sturner, S.; Elste, A.; Roytenberg, V.; Schwartz, J.H.; E
Neuron: 1, 833-864, 1988
A;Title: Two catalytic subunits of CAWD-dependent protein kinase generated by alternativ
A;Reference number: S19027, MUD: 90166564; PMID: 2483106
A;Retaus: preliminary
A;Molecule type: mRNA
A;Retaus: preliminary
A;Molecule type: mRNA
A;Retaus: preliminary
A;Note: the authors translated the codon AAC for residue 29 as Asp, GAC for residue 45 as Glu, CTA for residue 27, as Glu, AAC for residue 285 as Asp, and AAC for residue 288
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: protein kinase homology <KIN>
                                                                                                                                                                                                                                                              238
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     PSGNDDTDSEKSPEEVSGVVGIEDFEVLKVVGQGAFGKVYQVRKKDTSEIYAMKVMRKDK 175
                                                                                                                                                        KEETVKLPICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDPNIAAMLPRETQIT 178
                                                                                                                                                                                   239 ETTVVIYPSAWSQEMVSLLKKLLEPNPDQRF----SQLSDVQNFPYMNDINWDAVFQKRL 294
                                                                                                                                                                                                                                                                                                                                                                                                          350 -KDKIKLPQFVFNEAHALLKGLLQKEPERRLGSGPSGAEEIKKHKWFKAINWKKLEAREV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 DDFDRIKTLGTGSFGRVMLVQHKGESRNFYAMKILDKQKVVKLKQVEHTLNEKKILQSIN 101
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                                                                                   179 TMAGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKBIVHTF
                                                                                                                                                                                                                                                                                         80 HPFLVNLWYSFQDEBDMFMVVDLLLGGDLRYHLQQNVHFKBETVKLFICELVMALDYLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 QRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPEMFSSRKGAG
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24.1%; Score 507; DB 2; Length 352;
Best Local Similarity 33.3%; Pred. No. 4e-16;
Matches 108; Conservative 82; Mismatches 104; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 IPGFIPNKGRLNCDPTFE 312
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A;Accession: T28101
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Redidues: 1-375 <M12>
A;Coss-references: EMBL:282096; PIDN:CAB05035.1; GSPDB:GN00019; CESP:ZK909.2b
A;Experimental source: clone ZK909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-375 <WIL>
A;Croser references: EMBL:Z81511; PIDN:CAB04169.1; GSPDB:GN00019; CESP:ZK909.2b
A;Experimental source: clone F21F12
R;White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 ELQIMQGLEHPPLVNLWYSPQDEEDMFMVVDLLLGGDLRYHLQQNVHPKBETVKLFICEL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :|:| :: |||||::||:| ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 VMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPYMAPE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 MPSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFEITV---VTYPS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 AWSQEMVSLLKKGLEPNPDQRFSQL----SDVQNPPYMNDINWDAVFQKRLIPGFIPN-K 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 HFSNELKOLLKOLLKOVDLTKRYGNLKNGVADIKNHKWFGSTDWIAIYQKKIEAPPLPKCR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ZK909.2b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T21212; T28101
R;McLay, K.
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A;Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                           homology
                                                                                                                                                                                                                                                                                                                      14 ENEDVN----FDHFEILRAIGKGSFGEVCIVOKNDTKKMCAMKYMNKOKCVERNEVRNVFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOIMOGLEHPFLVNLWYSFODEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKLFICEL
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34.3%; Pred. No. 6.3e-16;
tive 74; Mismatches 103; Indels 22; Gaps
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                22;
A;Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3
C;Superfamily: kinase-related transforming protein; protein kinase
                                                                                                                                     Length 359;
                                                                                                                            Query Match 24.0%; Score 506; DB 2; Length 35:
Best Local Similarity 33.0%; Pred. No. 4.5e-16;
Matches 109; Conservative 78; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, November 1996 A; Reference number: 219391 A; Accession: T21212 A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 34.3%
Matches 104; Conservative
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A;Cross-references: GB:MG3311; NID:g191174; PIDN:AAA37010.1; PID:g191175
C;Comment: The Inactive enzyme contrains two regulatory chains and two catalytic chain:
Two types found in mammalian tissue are distinguished by having either type I or tyl
C;Comment: Both alpha and beta catalytic chains are found in many tissues, with the a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threomy bisomerally: kinase-related transforming protein; protein kinase homology c; Superfamily: kinase-related transforming protein; protein kinase homology c; Keywords: ATP; blocked amino end; cAMP-dependent, alpha catalytic chain #status predic F; 2-351/Product: protein kinase, cAMP-dependent, alpha catalytic chain #status predic F; 2-351/Product: protein kinase ATP-binding motif F; 2-38 Region: protein kinase ATP-binding motif F; 3/Modified site: myristylated amino end (GIV) (in mature form) #status predicted F; 3/Modified site: aspartic acid (Aan) #status predicted F; 3/Modified site: phosphate (Ser) (covalent) #status predicted F; 3,128,117,184/Binding site: Mg-ATP (Phe, GIV, GIU, GIU, Thr) #status predicted F; 3,92,167,169/Active site: Lys, GIU, ABP, Lys #status predicted F; 172,185/Binding site: magnesium (Aan, Asp) #status predicted F; 198/Binding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein kinase (EC 2.7.1.37), cAMP-dependent, alpha catalytic chain - Chinese hamster protein kinase (EC 2.7.1.37), cAMP-dependent, alpha catalytic chain - Chinese hamster C;Species: Cricetulus griseus (Chinese hamster) C;Dace: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jun-1999 C;Accession: B4038# R;Howard, P.; Day, K.H.; Kim, K.E.; Richardson, J.; Thomas, J.; Abraham, I.; Fleischm, J. Bio, Chem. 266, 10189-10195, 1991 A;A;Title: Decreased catalytic subunit mRNA levels and altered catalytic subunit mRNA s:A;Reference number: A40384; MUID:91244783; PMID:1645343
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                                                                                                                                                                                                                                                     269 HFSNELKOLLKANLLQVDLTKRYGNLKNGVADIKNHKWFGSTDWIAIYQKKITPPSF-SKG 327
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                                                  217
                                                                                                                                           VMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTWAGTKPYMAPE 190
                                                                                                          191 MFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTV---VTYPS 247
                                                                                                                                                                                                                       248 AWSQEMVSILIXKILEPNPDQRFSQL----SDVQNFPYMNDINWDAVFQKRLIPGFIPNKG 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 DHFDRIKTLGTGSFGRVMLVKHKGTGNHYAMKILDKQKVVVKLKQIEHTLNBKRILQAVNF
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                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-351 <HOW>
                                                                                                                                                                                                                                                                                                                                                                                             328 ESN 330
                                                                                                                                                                                                                                                                                                                                        RLN 306
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A;Molecule type: DNA
A;Residues: 1-823 <MAC>
A;Residues: 1-823 <MAC>
A;Residues: 1-823 <MAC>
A;Residues: 1-823 <MAC>
A;Residues: 1-824 <MAC>
A;Residues: 1-825 <MAC>
A;Cross-references: EMBL: U00029; NID:g551322; PIDN:AAB69735.1; PID:g458923; MIPS:YHR205w
B;di Blasi, F.; Carra, E.; de Vendittis, E.; Masturzo, P.; Burderi, E.; Lambrinoudaki, I
Yeast 9, 21-32, 1993
A;Title: The SCH9 protein kinase mRNA contains a long 5' leader with a small open readin
A;Reference number: S30021; MUID:93182531; PMID:8442384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
Ksteywords. ATP; phosphotransferase; serine/threonine-specific protein kinase
F;409-670/Domain: protein kinase homology <RIN>
F;417-425/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:857629; NID:95277; PIDN:CA440853.1; PID:95279
A;Notes: The nucleotide sequence was submitted to the EMBL Data Library, February 1991
A;Nota, T.; Cameron, S.; Sass, P.; Wigler, M.
Genes Dev. 2, 517-527, 1988
A;Title: SCH9, a gene of Saccharomyces cerevisiae that encodes a protein distinct from, A;Reference number: A28429; MUID:88255839; PMID:3190050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 DIRYHLQQNVHFKEETVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 IA-AMLPRETQITTMAGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 RSSTSSKEIVHTFETTVVTYP-SAWSQEMVSLLKKKLLEPNPDQRFSQLSD---VQNFPYM 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613 -- AENNOKMYOKIAPGKVKFPRDVLSÓEGRSFVKGLLNRNPKHRLGAIDDGRELRAHPFF 670
                                                      probable protein kinase SCH9 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
                                                                         NiAlternate names: protein YHR205w
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence revision 02-Dec-1994 #text_change 24-Sep-1999
C;Accession: 848986; S30022; A28429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 AMKYMNKOKCVERNEVRNVPKELQIM---QGLEHPFLVNLWYSPQDEEDMFMVVDLLLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 502.5; DB 2; Length 823;
; Pred. No. 1.3e-15;
68; Mismatches 113; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRKPPVFDE--NEDVNF-------DHFBILRAIGKGSFGEVCIVQKNDTKKMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
Residues: 'M',1-364,'S',366-749,'K',751-823 <TOD>
:Cross-references: EMBL:X12560; NID:g4425; PIDN:CAA31073.1; PID:g4426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S30022
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                           submitted to the EMBL Data Library, February 1994
Albestription: The sequence of S. cerevisiae cosmid 9177.
AlBeference unmber: $46671
Albecession: 848986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: SGD:S0001248; MIPS:YHR205w Map position: 8R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.9%;
Best Local Similarity 35.3%;
Matches 118; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
Residues: 'M',1-823 <DIB>
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Search completed: June 25, 2004, 10:50:09 Job time: 22 secs

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Sequence 158, App
Sequence 4, Appli
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Sequence 5, Appli
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Sequence 2, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 30, Appli
Sequence 33, Appli
Sequence 32, Appli
                                                                                                     June 25, 2004, 10:50:15; Search time 48 Seconds (without alignments) 2329.088 Million cell updates/sec
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1: /cgm2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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18: /cgm2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
18: /cgm2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-074-978A-158
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2 US-10-667-442-2

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US-09-841-683-11

2 US-10-362-892-20

2 US-10-182-243-33

5 US-10-182-243-33

5 US-10-410-764-101

US-09-841-683-9
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US-10-667-442-4
US-10-254-869-4
US-09-801-876B-5
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                            1163542 seqs, 282313646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
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seq length: 200000000
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Sequence 2, Application US/09801876B

Sequence 2, Application US/09801876B

Patent No. US20020127683A1

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/801,876B

CURRENT PILING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FactsEQ for Windows Version 4.0

SEQ ID NO 2

TYPE: RR
Sequence 5, Appli
Sequence 15, Appli
Sequence 15, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 6, Appli
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100.0%; Score 2104; DB 9; Length :
Best Local Similarity 100.0%; Pred. No. 5e-169;
Matches 396; Conservative 0; Mismatches 0; Indels
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1 US-10-254-869-5
1 US-10-10-34-318-356
1 US-10-10-14-978A-157
1 US-10-10-14-978A-157
1 US-10-10-156-14
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RESULT 2
(Sequence 2, Application US/10667442)
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(Seural INFORMATION:
(SEXERAL INFORMATION:
(SEXERAL INFORMATION: SOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: 1 THEREOF TITLE OF INVENTION: 1 THEREOF TITLE OF INVENTION: 2003-09-23
(CURRENT APPLICATION NUMBER: US/10/667,442)
(CURRENT FILING DATE: 2003-09-23
(NUMBER OF SEQ ID NOS: 8
(SOFTWARE: FREEESEQ for Windows Version 4.0)
(SEQ ID NO 2)
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181 AGTKPYMAPEMPSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET 240
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Publication No. US20030027307A1
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-667-442-2
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APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
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APPLICANT: Nepomnichy, Gregory
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Walke, D. Wade
TITLE OP INVENTION: No. US20020081600Alel Human Kinase Proteins and Polynucleotide
FILE REFERENCE: LEX-0167-USA
CURRENT APPLICATION NUMBER: US 60/199,499
PRIOR PILING DATE: 2000-04-25
PRIOR PELING DATE: 2000-06-01
PRIOR PELING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 12
SOPINARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 396
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1160DIV
CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8
SOFTMARR: PASLESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 396
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100.0%; Score 2104; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 5e-169;
Matches 396; Conservative 0; Mismatches 0; Indels 0;
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Patent No. US20020081600A1
GENERAL INFORMATION:
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US-10-254-869-2
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                                                                                                                                                                                                                                                                                                                                                                         Length 396;
                                                                                                                                                                                                                                                                     ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040038881A1 7946584CD1
US-10-362-892-20
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Pred. No. 9.3e-168;
1; Mismatches 1;
                                 60/240,542
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60,
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PERL Program
SEQ ID NO 20
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.5%;
Matches 394; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
LENGTH: 396
TYPE: PRT
ORGANISM: Home sapiens
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                Length 396;
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                                                       Score 2089; DB 9;
Pred. No. 9.3e-168;
1; Mismatches 1;
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APPLICANT: LAL, Preet G.; RAKUMAR, JAYAIR
APPLICANT: WARREN, Bridget A.; KEARNEY, Lia
APPLICANT: WARREN, Bridget A.; KEARNEY, Lia
APPLICANT: BURECRD, Neil
TITLE OF INVENTION: HUMAN KINASES
FILE RERERENE: P-0.209 USN
CURRENT APPLICATION NUMBER: USN
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 60/229,873
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR PLING DATE: 2000-09-31
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-14
PRIOR PLING DATE: 2000-09-14
PRIOR PLING DATE: 2000-09-14
PRIOR PLING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US 60/234,902
PRIOR PLING DATE: 2000-09-29
PRIOR PLING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/236,499
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Publication No. US2004003881A1
GENERAL INFORMATION:
                                                       Ouery Match
Best Local Similarity 99.5%;
Matches 394; Conservative
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     US-09-841-683-11
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US-10-182-243-33

US-10-182-243-33

Sequence 33, Application US/10182243

Publication No. US20040048310A1

GENERAL INFORMATION:
APPLICANT: PLOWMAN' GREGORY D.
APPLICANT: MANNING, GERARD
APPLICANT: MANNING, GERARD

APPLICANT: MANNING, GERARD

TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE

TITLE OF INVENTION: ENZYMES

TITLE OF INVENTION: ENZYMES

CURRENT APPLICATION NUMBER: US/10/182,243

CURRENT FILING DATE: 2001-01-25

PRIOR FILING DATE: 2001-01-25
                                                      301 NKGRINCDPTFELERMILESKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLDSVQKEFI 360
301 NKGRINCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLDSVQKEFI 360
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                                                                          1 MGANTSRKPPVFDENEDVNFDHFBILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
                                                                                                                           1 MGANTSRKPPVPDENEDVNPDHPEILRAIGKGSFGKVCIVQKNDTKKMYAMKYMNKQKCV
                             Gape
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APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
APPLICANT: YAO, Wonique G.; GANDHI, Ameena R.;
APPLICANT: YAO, Wonique G.; GANDHI, Ameena R.;
APPLICANT: GATTERSON, Chandra; VUB, Henry;
APPLICANT: BAUGHN, Marhah R.; TRIBOULEY, Catherine M.;
APPLICANT: HOWNTON, Maindel; ELLIOTT, Vicki S.;
APPLICANT: HOWNTON, Janice; TANG, Y. TOM;
APPLICANT: HOWNTON, Janice; TANG, Y. TOM;
APPLICANT: AL'ANDAL, Janice, TANG, Y. TOM;
APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
APPLICANT: LU, DYUNG Aliam M.; Lall, Preedti G.;
APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
TITLE OF INVERTION: HUMAN KINASES
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Best Local Similarity 99.5%; Pred. No. 9.3e-168;
Matches 394; Conservative 1; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/288,798

CURRENT FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: PCT/US01/27219

PRIOR PILING DATE: 2001-08-31

PRIOR PLILING DATE: 2000-10-13

PRIOR PLILING DATE: 2000-10-06

PRIOR PLILING DATE: 2000-10-06

PRIOR PLILING DATE: 2000-10-06

PRIOR PLILING DATE: 2000-09-29

PRIOR PLILING DATE: 2000-09-14

PRIOR PLILING DATE: 2000-09-14

PRIOR PLILING DATE: 2000-09-14

PRIOR PLILING DATE: 2000-09-14
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FILING DATE: 2000-08-31
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Publication No. US20030207299A1
GENERAL INFORMATION:
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APPLICANT: Meyers, Rachel B.
APPLICANT: Meyers, Rachel B.
APPLICANT: MacBeth, Kyle J.
APPLICANT: MacBeth, Kyle J.
APPLICANT: MacBeth, Kyle J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Radolph-Owen, Laura A.
APPLICANT: Rapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Carroll, Joseph M.
APPLICANT: Carroll, Joseph M.
APPLICANT: Applicant: Carroll, Joseph M.
APPLICANT: TILL OF INVENTION: 25199, 3330, 33949, 47148, 50226,
TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
TITLE REFERENCE: MINJEST ON UNMBER: US/10/410,764
CURRENT APPLICANTON NUMBER: 2203-04-10
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                                                                                                                   PEATURE:
NAME/KEY: misc feature
PEATURE INFORMATION: Incyte ID No. US20030207299A1 7946584CD1
US-10-288-798-20
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PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR PLICATION NUMBER: US 09/966,614
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                                                                          TYPE: PRT
ORGANISM: Homo sapiens
SOFTWARE: PERL Program
SEQ ID NO 20
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-410-764-101
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                                                                                                                                                                                                                                                                                                                                                                                     1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGKVCIVQKNDTKKMYAMKYMKQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 BRNEVRNVPKELQIMQGLEHPFLVNLWYSPQDBEDMPMVVDLLLGGDLRYHLQQNVHPKE
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                                                                                                                                                                                                                                                                                                                                                  1 MGANTSRKPPVFDENEDVNFDHFBILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCV
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US-10-108-260A-2674
; Sequence 2674, Application US/10108260A
; Sequence 2674, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2674
; LENGTH: 258
                                                                                                                                                                                                                               Length 407;
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Best Local Similarity 99.4%; Pred. No. 1.3e-144;
Matches 342; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                            Query Match 97.3%; Score 2047; DB 9;
Best Local Similarity 98.7%; Pred. No. 3.3e-164;
Matches 387; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 IFNREKVNRDFNKRQPNLALEQTKOPQVTNGQ 392
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         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9 LENGTH: 407
                                                                                                      TYPE: PRT
ORGANISM: homo sapiens
US-09-841-683-9
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CORGANISM: Homo sapiens
US-10-108-260A-2674
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Patent No. US20020081600A1

GENERAL INFORMATION:

APPLICANT: Hu, Yi

APPLICANT: Wang, Xiaoming

APPLICANT: Wang, Down

APPLICANT: Wang, Down

APPLICANT: Wang, Down

CURRENT PRILING DATE: 2001-04-24

PRIOR PELING DATE: 2001-04-24

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-05-01

PRIOR FILING DATE: 2000-05-01

WUMBER OF SEQ ID NOS: 12
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PRIOR PILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/238,054
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: US 10/281,094
PRIOR APPLICATION NUMBER: US 60/347,815
PRIOR PILING DATE: 2001-10-25
PRIOR PILING DATE: 2001-10-25
PRIOR PILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/369,440
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-764-101
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241 TVVTYPSAMSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIP 300
                                                                                     TVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIP 300
                                         181 AGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFET
  AGTKPYMAPEMFSSRKGAGYSPAVDWWSLGVTAYBLLRGRRPYHIRSSTSSKEIVHTFET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Smithson, Glennda
ITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                301 NKGRILNCDPTFELEEMILESKPLHKKKKRLAKGEKDMRKCDSSQ 344
                                                                                                                                                                       301 NKGRLNCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSSQ 344
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Taupier Jr, Raymond J
Moore, Wo. US20040010119A11le
Shenoy, Suresh
Edinger, Shlomit
Gunther, Erik
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CURRENT APPLICATION NUMBER: US/10/074,978A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: 60/268,221
PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/335,109
PRIOR FILING DATE: 2001-10-31
PRIOR PILING DATE: 2001-08-14
PRIOR PILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 60/268,496
PRIOR PILING DATE: 2001-02-13
PRIOR PAPLICATION NUMBER: 60/276,703
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-18
                                                                                                                                                                                                                                                                                                                          Sequence 158, Application US/10074978A Publication No. US20040010119A1 GENERAL INFORMATION:
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APPLICATION NUMBER: 60/310,797
FILING DATE: 2001-08-08
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FILING DATE: 2001-11-21
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Guo, Xiaojia (Sasha)
Fernandes, Elma
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Malyankar, Uriel M
Susev, Vladimir
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Ballinger, Robert
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Peyman, John
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Kekuda, Ramesh
Liu, Xiahong
Casman, Stacie
Boldog, Ferenc
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Heyes, Melvin P
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US-10-074-978A-158
181
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Sequence 4, Application US/09801876B
Sequence 4, Application US/09801876B
Barent No. US20020127683A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERRACE: CLOO1160
CURRENT APPLICATION NUMBER: US/09/801,876B
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 4.
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                                                                                                                                                                                                                                                                                                                     64; Indels 19; Gaps
PRIOR APPLICATION NUMBER: 60/268,646
PRIOR FILING DATE: 2001-02-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ. ID NOS: 547
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 158
LENGTH: 414
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Best Local Similarity 69.5%; Pred. No. 6.4e-112;
Matches 278; Conservative 38; Mismatches 64;
                                                                                                                                                                                                                                                                     Query Match

68.3%; Score 1437.5; DB 1

Best Local Similarity 69.7%; Pred. No. 8.6e-113;

Matches 278; Conservative 38; Mismatches 64;
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US-09-801-876B-4
                                                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
US-10-074-978A-158
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TYPE: PRT
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US-09-801-876B-5

Sequence 5, Application US/09801876B

Sequence 5, Application US/09801876B

Sequence 5, Application US/09801876B

GENERAL INFORMATION:

APPLICANT: YB, Jane et al

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

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TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
                                                                                                                                            Sequence 4, Application US/10254869

Publication No. US20030027307a1

Publication No. US20030027307a1

Publication No. US20030027307a1

APPLICANT: VE. Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO01160DIV

CURRENT PILIG DATE: 2002-09-26

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4
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     357 KBFIIFNREKVNRDFNKRQPNLALEQTKDPQGEDGQNNNL 396
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ORGANISM: Mus Musculus
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Publication No. US20040043466A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REPERBNCE: CLOOLISCOLY II
CURRENT APPLICATION NUMBER: US/10/667,442
CURRENT FILING DATE: 2003-09-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRABESEQ for Windows Version 4.0
SEQ ID NO 4
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Best Local Similarity 69.5%; Pred. No. 6.4e-112;
Matches 278; Conservative 38; Mismatches 64; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEFIIFNREKVNRDFNKRQPNLALEQTKDPQGEDGQNNNL 396
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US-10-667-442-4
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181 AGTKPYMAPEMPS--SRKGAGYSPAVDWWSLGVTAYBLLRGRRPYHIRSSTSSKEIVHTF 238
                                                             Length 403;
                                                77; Indels
                                DB 9;
                              Query Match 67.8%; Score 1425.5; DB 9 Best Local Similarity 68.2%; Pred. No. 8.5e-112; Matches 275; Conservative 44; Mismatches 77;
; TYPE: PRT
; ORGANISM: Human
US-09-801-876B-5
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241 KVERVHYSSTWCKGMVALLRKLITKDPESRVSSLHDIQSVPYLADMNWDAVFKKALMPGF 300 301 VPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKARARSRDGTKDSCPLNGHLQHCLETVRE 360 ETTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGF 298 299 IPNKGRLINCDPTFELBEMILESKPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDSVQK 357 358 EFIIFNREKVNRDFNKRQPNLALEQTKDPQG----EDGONNNL 396 239 ò g ઠે ð

Search completed: June 25, 2004, 10:56:33 Job time : 49 secs

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1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/laa/FUTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-801-876B-4
US-09-801-876B-5
US-09-801-876B-5
US-09-801-876B-6
US-09-819-607-4
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Listing first 45 summaries
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Sequence 18, Appl Sequence 38, Appl Sequence 6, Appl Sequence 6, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 10, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl	S, NUCLEIC N KINASE PROTEINS, AND USES	4; DB 4; Length 396; 1.6e-194; hes 0; Indels 0; Gaps 0; KGSFGEVCIVOKNDTKKMCAMKYMKOKCV 60
5 PCT-US94-10487-18 4 US-09-394-455-38 4 US-09-457-0408-37 4 US-09-457-0408-6 1 US-09-417-197-69 1 US-08-421-817-20 1 US-08-454-439-20 5 PCT-US94-10487-20 5 US-07-857-2248-7 1 US-08-221-817-19 1 US-08-221-817-19 1 US-08-221-817-19 1 US-08-454-439-15 1 US-08-454-439-15 1 US-08-454-439-15 1 US-08-454-439-15 1 US-08-454-439-15 1 US-08-454-439-15 1 US-08-454-439-15 2 US-07-980-526-2 1 US-08-454-439-15 1 US-08-454-439-15	ALIGNMENTS in US/09801876B it all SOLATED HUMAN KINASE PROTEINS ACID MOLECULES ENCODING HUMAN 1.60 1.00 1.00 1.00 2.001-03-09 2.001-03-09 2.001-03-09 2.001-03-09 2.001-03-09 2.001-03-09 2.001-03-09 2.001-03-09 2.001-03-09	*; Score 2104; D  *; Pred. No. 1.6e  0; Mismatches  VNFDHFEILRAIGKGSFG
93.5 92.5 92.5 92.5 92.5 92.5 92.5 92.5 92.5 92.5 92.5 92.5 93.5	1768-2 2, Applicatio 3, 6492155 NFORMATION: INVENTION:	rn 10
80000000000000000000000000000000000000	RESULT 1 US-09-801-876B-2 ; Sequence 2, App ; Patent No. 6492 ; GENERAL INFORMA ; APPLICANT: YE, ; TITLE OF INVEN; ; CURRENT APPLIC ; SQ ID NO 2 ; SQ ID NO 2 ; SQ ID NO 2 ; SQ ID NO 3 ; SQ ID NO 4 ; SQ ID NO 4 ; SQ ID NO 4 ; SQ ID NO 5 ; TYPE: PRT	Query Match Best Local best Local by Matches 396 Oy 121 Oy 121 Oy 121 Oy 181 Oy 181 Oy 241 Oy 241 Ob 241 Oy 301 Oy 301 Oy 301 Oy 351 Oy 351

us-10-667-442-2.rai

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APPLICANT: Nepomalchy, Borie
APPLICANT: Nepomalchy, Borie
APPLICANT: Nepomalchy, Stateming
APPLICANT: New Manage Mission
APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Walke, D. Wade
TITLE OF INVENTION NO. 6617-USA
CURRENT APPLICATION NUMBER: US/09/841,683
CURRENT FILING DATE: 2001-04-24
FRIOR APPLICATION NUMBER: US 60/199,499
FRIOR APPLICATION NUMBER: US 60/201,227
FRIOR APPLICATION NUMBER: US 60/201,227
FRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PRECE OF Windows Version 4.0
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
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Pred. No. 5.1e-189;
2; Mismatches 3;
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99.3%; Score 2089; DB 4;
Best Local Similarity 99.5%; Pred. No. 4.4e-193;
Matches 394; Conservative 1; Mismatches 1;
PRIOR APPLICATION NUMBER: US 60/201,227
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 396
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; Sequence 9, Application US/09841683
; Patent No. 6617147
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Best Local Similarity 98.7%;
Matches 387; Conservative 2
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APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
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CRGANISM: homo sapiens
US-09-841-683-9
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: homo sapiens
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US-09-841-683-11
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                                                                                                         RESULT 2
US-10-254-669-2
US-10-254-669-2
i Sequence 2, Application US/10254869
i Patent No. 6651117
i GENERAL INFORMATION:
i APPLICANT: YE, Jane et al
i TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
i TITLE OF INVENTION: THEREOF
i TITLE OF INVENTION: THEREOF
i TITLE OF INVENTION: US/10/254,869
i CURRENT APPLICATION NUMBER: US/10/254,869
i CURRENT FILING DATE: 2002-09-26
in NUMBER OF SEQ ID NOS: 8
i SOFTWARE: FaetSEQ for Windows Version 4.0
i SEQ ID NO 2
i EMEGYTH: 396
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100.0%; Score 2104; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.6e-194;
Matches 396; Conservative 0; Mismatches 0; Indels 0.
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           361 IFNREKVNRDFNKRQPNLALEQTKDPQGEDGQNNNL 396
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Patent No. 6617147
GENERAL INFORMATION:
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CRGANISM: Human
US-10-254-869-2
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 FIPNKGRINCDPTFELEEMILESKPLHKKKKRLAK-KEKDMRKCDSSQTCLLQEHLDSVQ 356
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; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-4
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US-10-254-869-4
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APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOLISO
CURRENT PAPLICATION NUMBER: US/09/801,876B
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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                                                                  ERNEVRIVEKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKE 120
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                                                                                   RENEVRIVV PKELQIMQELEH PFLVNI MYS FQDEEDMFMVVDLILGGDLRYHLQQINV HPKE
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MGANTSRKPPVPDENEDVNPDHFEILRAIGKGSPGEVCIVQKNDTKKMCAMKYMNKQKCV
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Best Local Similarity 69.5%; Pred. No. 3e-129;
Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps
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; Patent No. 6492155
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CORGANISM: Mus Musculus
US-09-801-8768-4
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US-09-801-876B-4
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Sequence 4, Application US/10254869
Patent No. 6653117
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOO11601UV
CURRENT APPLICATION NUMBER: US/10/254,869
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Faster of for Windows Version 4.0
SEQ ID NO 4
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Patent No. 6492155
GENERAL INFORMATION:
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CL001160
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, ORGANISM: Homo sapiens
US-09-799-875-14
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; Sequence 5, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: DATE: 2002-09-26
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT PILLING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; TYPE: PRT
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                                                                                                                                                                                                                                                                              ERNBVRNVPKELQIMQGLEHPFLVNLMYSPQDEEDMFMVVDLLLGGDLRYHLQQNVHFKE
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                                                                                                                                                                                     DB 4; Length 403;
                                                                                                                                                                                   Query Match 67.8%; Score 1425.5; DB 4; Length Best Local Similarity 68.2%; Pred. No. 4.1e-129; Matches 275; Conservative 44; Mismatches 77; Indels
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; CURRENT APPLICATION NUMBER: US/09/801,876B; CURRENT FILING DATE: 2001-03-09; NUMBER OF SEQ ID NOS: 8; SCTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 5; LENGTH: 403; TYPE: PRT ; CRGANISM: Human US-09-801-876B-5
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                                                  121 BTVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRBTQITTM 180
61 BRDEVRNVFRELQIMQGLEHPFLVNLWYSPQDEEDMFWVVDLLLGGDLRYHLQQNVHFTE 120
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                                                                                                                                                   181 AGTKDYMAPEMFS--SRKGAGYSFAVDWMSLGVTAYELLRGRRPYHIRSSTSSKEIVHTF
                                                                                                                                                                                                                                                        239 ETTVOTYPSAMSOEMVSLLKKLLEPNPDQRFSQLSDVONPPYMNDINWDAVFOKRLIPGF
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APPLICANT: Meyels, Rachel
APPLICANT: Machalon, Mark
APPLICANT: Walliamann, Mark
TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
TITLE OF INVENTION: Therefor
FILE REPERENCE: 35800/20996
CURRENT APPLICATION NUMBER: US/09/799,875
CURRENT PILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 60/182,059
PRIOR APPLICATION NUMBER: 09/659,287
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 14
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Best Local Similarity 64.5%; Pred. No. 2.7e-119;
Matches 254; Conservative 53; Mismatches 77; Indels 10;
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; Sequence 14, Application US/09799875
; Patent No. 6638721
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APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOLI60
CURRENT APPLICATION NUMBER: US/09/801,876B
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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Patent No. 6653117
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES
TITLE OF
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                                                                                                                                               364 QDFVIFNREKL----KRSQDLPREPLPAPESRD 392
                                                                                                  357 KEPIIFNREKVNRDPNKROPNLALEQTKDPOGED 390
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Best Local Similarity 64.34
Matches 250; Conservative
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US-09-801-876B-6
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US-10-254-869-6
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Sequence 4, Application US/09819607

Patent No. 6686176

GENERAL INFORMATION:
APPLICANT: BRASLEY: Blien et al
APPLICANT: BRASLEY: Blien et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TILE REPERENCE: CLOOL1078

CURRENT APPLICATION NUMBER: US/09/819,607

CURRENT PILING DATE: 2001-03-29
NUMBER: OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4
LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                61 RNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SARRPVFDDKEDVNFDHPQILRAIGKGSFGKVCIVQKRDTEKMYAMKYMNKQQCIERDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 YMAPEMFSS---RKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 VNPDHPEILRAIGKGSFGEVCIVQXNDTKKMCAMKYMNKQKCVERNEVRNVFKELQIMQG
                                                                                                                                                                                                                                                                                6 BRKPPVPDENEDVNPDHPBILRAIGKGSFGEVCIVQKNDTKKMCAMKYMNKQKCVBRNEV
                                                                                                                                                                                                                                                                                                                                                                          66 RNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFKEETVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 PICELVMALDYLONORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 TYPSAWSQEMVSLLKKLLBPNPDQRFSQLSDVQNPPYMNDINWDAVFQKRLIPGFIPNKG
                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                    DB 4; Length 384;
                                                                                                                                                                                 Query Match 62.6%; Score 1317.5; DB 4; Length Best Local Similarity 64.3%; Pred. No. 9.9e-119; Matches 250; Conservative 54; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 FNREKVNRDFNKROPNLALEQTKDPQGED 390
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361 FNREKL----KRSQELMSEPPPGPETSD 384
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 6
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                                                                                       TYPE: PRT
ORGANISM: Mus Musculus
US-10-254-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus US-09-819-607-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Best Local Simil
Matches 243; (
                                                                      LENGTH: 384
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APPLICANT: Hu, Yi.
APPLICANT: Nepomnichy, Boris
APPLICANT: Nepomnichy, Soris
APPLICANT: Nepomnichy, Soris
APPLICANT: Nepomnichy, Gregory
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encodi:
FILE REPERBNCE: LEX-0167-USA
CURRENT PILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199, 499
PRIOR PILING DATE: 2000-04-25
PRIOR PLING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: AVINGWA VEISION 4.0
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Sequence 2, Application US/09819607

Patent No. 6686176

GENERAL INPORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REPERBNCE: CL001078

CURRENT APPLICATION NUMBER: US/09/819,607

CURRENT PILIDE OF DINOS: 5

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FREESE OF WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 BIVKLPICELVWALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRBTQITTM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERNEVRAVPEKELQIMQGLEHPPLAVALMYSPQDEEDMFMAVDLLLGGDLRYHLQQAVHFKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ERNEVRIVVFKELQIMQGLEHPPLVNLMYSPQDEEDMFMVVDLLLGGDLRYHLQQNVHFKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 BTVKLFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGANTSRKPPVFDENEDVNPDHPEILRAIGKGSFGEVCIVQKONDTKKMCAMKYMNKQKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGANTSRKPPVPDENEDVNPDHFBILRAIGKGSFGKVCIVQKNDTKKMYAMKKPKNKV
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54.1%; Score 1137.5; DB 4; Length 369;
Best Local Similarity 62.8%; Pred. No. 2.1e-101;
Matches 218; Conservative 47; Mismatches 73; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVTAYBLLRGR 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1158; DB 4;
Pred. No. 1.1e-103;
1; Mismatches 1;
                                     Sequence 5, Application US/09841683
Patent No. 6617147
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%;
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Best Local Similarity 99.1
Matches 218; Conservative
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Human
US-09-819-607-2
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LENGTH: 369
TYPE: PRT
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LENGTH: 225
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APPLICANT: Wary Xiaoming
APPLICANT: Wary Xiaoming
APPLICANT: Bonoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Walke, John
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polymucleotides Encoding
FILE REPERENCE: LEX-0167-08A
CURRENT APPLICATION NUMBER: US 60/199,499
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR PLING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FRESSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTKPYMAPEMPSSRKGAGYSPAVDWWSLGVTAYELLRGRRPYHIRSSTSSKBIVHTFET 240
181 GGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEMVA 240
                                                                                                                                                                                                                                                                               256 LLKKGLLBPNPDQRFSQLSDVQNFPYMNDINWDAVFQKRLIPGFIPNKGRLNCDPTFBLEB 315
                                                                                                                                                                                           MILESKPLHKKKKRLAKKEKDMRKCDSSQT--CLLQEHLDSVQKEFIIFNREKVNRDFNK 373
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                                                                                KGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSSKEIVHTFETTVVTYPSAWSQEMVS
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Pred. No. 6.1e-104;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09841683
Patent No. 6617147
                                                                                                                                                                                                                                                                                                                                       374 ROPNLALEQTKDPOGED 390
                                                                                                                                                                                                                                                                                                                                                                               356 RSQELMSEPPPGPETSD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.2%;
Matches 222; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: homo sapiens
US-09-841-683-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-841-683-7
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181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLFKTLTVNPEHRLSSLQDVQAAPALAGVL 240
                                                                                                     168 AAMLPRETQITIMAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGVTAYELLRGRRPYHI 225
                                                        226 RSSTSSKEIVHTPETTVVTYPSAMSQEMVSLLKKTLEPNPDQRPSQLSDVQNPPYMNDIN 285
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